Protein Sequence Searches - February 2005

Il of the sequence databases on ABSS have recently been updated.

- permanent accession numbers. The new UniProt record may not contain the previous temporary numbers from the most recent version of UniProt. These sequences have been assigned new Please note that the curators of the UniProt database have purged some temporary accession accession number.
- extension .rup) that can no longer be found in the database, the permanent record with the new accession number can be found by searching the old accession number in the UniProt Protein If you encounter an accession number from an older search run against UniProt (results file Archive database (UniPARC) at:

http://www.pir.uniprot.org/database/archive.shtm

If you have any questions regarding this information or your results, please contact any STIC searcher

When submitting sequence search results for scanning into IFW, please members of the public who may encounter UniProt temporary accession include a copy of this attachment to assist any future Examiners or

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66 LEWMGGIIPIFGTANYAQKFQGRVTITADESTSTAYMELSSLRSEDTAVYYCARD---- 120
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Ishibashi T., Kanehori K., Yosida M., Watanabe S., Ishida S., Ono Y.,
Hotuta T., Hizacka S., Murakawa K., Takiguchi S., Kusano J.,
Hotuta T., Hizacka S., Murakawa H., Ishida M., Yamashita H., Chiba Y.,
Suzuki Y., Hata H., Nakagawa K., Mizuno S., Morinaga M., Kawamura M.,
Sugiyama T., Irie R., Otsuki T., Sato H., Nishikawa T., Sugiyama A.,
Kawakami B., Nagai K., Isogai T., Sugano S.;
Submitted (OCT-2001) to the EMBL/GenBank/DDBJ databases.
EMBL, AKOS0027, BAB71633.1; --
HSSP; P01876; 10W0
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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InterPro; IPR031909; Ig_cl.
InterPro; IPR003806; Ig_w.
InterPro; IPR003806; Ig_w.
Pfam; PF00449; Cl.set; 2.
Pfam; PF00447; ig; 1.
SMART; SM00406; IGV.
PROSITE; PS00390; IG_LIKE; 4.
PROSITE; PS00290; IG_MHC; UNKNOWN_1.
SEQUENCE 496 AA; 53532 MW; C72EE1E247C86FED CRC64;
                                                                                                                                                                                                                                                            096DX0
096DX0;
01-DEC-2001 (TrEMBLrel. 19, Created)
01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
Hypothetical protein FLJ25298.
Homo sapiens (Human)
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Q8K0Z4
Q91WT3
Q99LA6
Q99LA6
Q8VCV5
Q91WP5
Q6PDB8
Q91X92
Q8VEAQ
Q91X77
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SEQUENCE FROM N.A.
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Copyright (c) 1993 - 2005 Compugen Ltd.
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A Klausner R.L., Feingold E.A., Grouse L.H., Derge J.G.,
A Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
A Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
Hopkins R.F., Jordan H., Moore T., Max S.I., Warng J., Hsieh F.,
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A Altschul S.F., Zeeperg M.B., Bonaldo M.F., Casrinci P., Hong L.,
Brownstein M.J., Usdin T.B., Toshiyuki S., Carrinci P., Prange C.,
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Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunzarne P.H.,
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A Nilalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
Richards S., Worley K.C., Hale S., Garchenko Y., Bouffard G.G.,
Multing M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
A Rodiguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
A Dones S.J., Marra M.A.,
T. "Generation and initial analysis of more than 15,000 full-length human
                                                 CPVPSTPPTPSPSTPPTPSPSCCHPRLSLHRPALEDLLLGSEANLTCTLTGLRDASGVTF 303
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                    CPVPSTPPTPSPSTPPTPSPSCCHPRLSLHRPALEDLLLGSEANLTCTLTGLRDASGVTF
                                                                                                                 TWTPSSGKSAVQGPPDRDLCGCYSVSSVLSGCAEPWNHGKTFTCTAAYPESKTPLTATLS
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Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
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Submitted (ARR-2001) to the EMBL/GenBank/DDBJ databases.
EMBL; BC005931, AAH05931.1;
HSSP; PO1876; 10W0.
InterPro; IPR007110; Ig-like.
InterPro; IPR003597; Ig_c1.
InterPro; IPR003596; Ig_WHC.
InterPro; IPR003596; Ig_WHC.
InterPro; IPR003596; Ig_V.
Ffan; PF07654; C1-set; Z.
Pfan; PF07064; ig_i1.
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Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002)
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PROSITE; PS50835; IG_LIKE; 4.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             246 PSPSTPPTPSPSCCHPRLSLHRPALEDLLLGSEANLTCTLTGLRDASGVTFTWTPSSGKS
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                                                                                                                                       Gaps
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Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
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                                                                                  DB 2; Length 500;
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Zheng S., Shao X., Cao J., Geng L., Fang Y., Dong Q.;

Zheng S., Shao X., Cao J., Geng L., Fang Y., Dong Q.;

Submitted (JUN-2000) to the EMBL/GenBank/DDBJ databases.

EMBL, ARJS987.1; -.

HSPP, P01876; 10W0.

Pfam; PF07654; C1-set; 2.

SMART; SMO0406; IGV; 1.

PROSITE; PS00290; IG LIKE; 4.

PROSITE; PS00290; IG LIKE; 4.

SEQUENCE 497 AA; 53665 WW; F24D08DFASA663E5 CRC64;
PROSITE; PS00290; IG MHC; UNKNOWN 1.
SEQUENCE 500 AA; 54154 MM; 0A9BF43F2A3CC6D9 CRC64;
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01-WAR-2002 (TrEMBLrel. 20, Last sequence update)
01-WAR-2004 (TrEMBLrel. 26, Last annotation update)
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                                                                            87.9%; Score 2295.5; DB 2
89.5%; Pred. No. 6.1e-130;
ive 14; Mismatches 24;
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Matches 431; Conservative
                                                                                                     Best Local Similarity 89.5
Matches 433; Conservative
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TISSUE=Mammary gland;
    SEQUENCE FROM N.A.
TISSUE=Blood;
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MEDINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
MA Klausher R.D., Colling F.S., Wagner L., Shenmen C.M., Schuler G.D.,
Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
A plokins R.F., Jordan H., Moore T., Max S.I., Wang J., Habie F.,
Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
Rabi chenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
Rapleton M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
Robards S.A., McEwan P.J., McKernan K.J., Makek J.A., Gunararne P.H.,
Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
A Villalon D.K., Muxny D.M., Madan A., Rodiigues S., Sanchez A.
Mhiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
A Matseiley R.W., Touchman J.W., Green E.D., Dickson M.C.,
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T. "Generation and initial analysis of more than 15,000 full-length human
RT and mouse CDNA sequences.";
P. Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
                                                                                                                                                                 171
                                                                                                                                                                                          124 RGFGYNWFDP----WGHGTLVTVSSASPTNPKVFPLSLCSTQPDGNVVIACLVQGFFPQE 179
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SGVTFTWTPSSGKSAVQCPPERDLCGCYSVSSVLPGCAEPWINGKTFTCTAAYPESKTPL 359
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                           63
LEWMGGIIPIFGTANYAQKFQGRVTITADESTSTAYMELSSLRSEDTAVYYCAR----
                                                                                                                                                                   -----DPFLHYWGQGTLVTVSTASPTSPKVFPLSLCSTQPDGNVVIACLVQGFFPQE
                                                                                                                                                                                                                                                               PLSVTWSESGQGVTARNFPPSQDASGDLYTTSSQLTLPATQCLAGKSVTCHVKHYTNPSQ
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    YLTWASRQEPSQGTTTFAVTSILRVAAEDWKKGDTFSCMVGHEALPLAFTQKTIDRLAGK
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01-0CT-2002 (TrEMBLrel. 22, Last sequence update)
01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
MGC27165 protein.
MGC27165 protein.
Eukaryota; Metazoa; Chordata; Craniata, Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          183 LSVTWSESGGGVTARNFPPSQDASGDLYTTSSQLTLPATQCLAGKSVTCHVKHYTNPSQD 242
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            123 CSGGSCLGYYMDVWGKGTTVTVSSASPTSPKVPPLSLCSTQPDGNVVIACLVQGFFPQEP 182
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              VTVPCPVPSTPPTPSPSTPPTPSPSCCHPRLSLHRPALEDLLLGSEANLTCTLTGLRDAS 292
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            243 VTVPCPVPSTPPTPSPSTPPTPSPSCCHPRLSLHRPALEDLLLGSEANLTCTLTGLRDAS 302
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                                                                                                                                                                                                                                                                                                                                                                                                                               DB 2; Length 499;
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Strausberg R.;
Submitted (JUN-2002) to the EMBL/GenBank/DDBJ databases.
EMBL BC032249; AAH32249.1; --
HSSP; P01876; 10W0.
                                                                                                  InterPro; IPR01310; Ig-like.
InterPro; IPR03597; Ig_c1.
InterPro; IPR003506; Ig_MHC.
InterPro; IPR003506; Ig_V.
Pfam; PF00647; Ig. 1.
SWART; SM00407; ig; 1.
PROSITE; PS50835; IG_LIKE; 4.
PROSITE; PS50835; IG_LIKE; 4.
PROSITE; PS002500; IG MHC; UNXNOWN 1.
SRQUENCE 499 AA; 53376 MW; 93ASC89582054F32 CRC64;
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Q96K68.
Q1-DEC-2001 (TrEMBLrel. 19, Created)
O1-DEC-2001 (TrEMBLrel. 19, Last sequence update)
HAR-2004 (TrEMBLrel. 26, Last annotation update)
Hypothetical protein FL114473.
Homo sapiens (Human)
                                                                                                                                                                                                                                                                                                                                                                                                                      Match 85.2%; Score 2224.5; DB 2 Local Similarity 83.9%; Pred. No. 1.1e-125; les 417; Conservative 26; Mismatches 41;
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Matches 420; Conservative
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SEQUENCE FROM N.A.
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             Actual T., Suzuki Y., Nishikawa T., Otsuki T., Sugiyama T., Irie R., Makamatsu A., Hayashi K., Sato H., Nagai K., Kimura K., Makita H., Sakhine M., Obayashi M., Nishi T., Shibahara T., Tanaka T., Ishii S., Ra Sekine M., Obayashi M., Nishi T., Shibahara T., Tanaka T., Ishii S., RA Yamamoto J., Saito K., Kawai Y., Isono Y., Nakamura W., Nagahari K., RA Murakami K., Yasuda T., Iwayanagi T., Wagatsuma M., Shiratori A., Radhara K., Kamihara K., Katsuta T., Kukwa E., Omura Y., RA Takahashi M., Kanda K., Ishibashi T., Yamashita H., Murakawa K., Fujimori K., RA Tanai H., Kimata M., Watanabe M., Hiraoka S., Chiba Y., Ishida S., RA Tanai H., Kimata M., Watanabe M., Hiraoka S., Chiba Y., Ishida S., RA Tanai H., Kimata M., Watanabe M., Hiraoka S., Chiba Y., Ishida S., RA Togiya S., Komai F., Hara R., Takeuchi K., Arita M., Imose N., RA Musashino K., Yuuki H., Oshima A., Sasaki N., Aotsuka S., Senoh A., Mizoguchi H., Golima A., Sasaki N., Rawakami B., Makagawa S., Senoh A., Mizoguchi H., Goto Y., Shimizu F., Wakebe H., Rawabata R., Matanabe K., Kumagai A., Takenoto M., Kawakami B., Kawabata A., Hikiji T., Kobacake N., Inagaki H., Kawakami T., Kobacake N., Inagaki H., Kawakami T., Noguchi S., Itoh T., Shigeta K., Senba T., Rawabata A., Hikiji T., Kobacake N., Inagaki H., Matanabe M., Takhico H., Tanigami Y., Kawakami T., Oyama M., Hata H., Watanabe M., Komatsu T., Kobacake N., Inagaki H., Matanabe T., Sugiyama M., Sasaki M., Augesahi T., Oyama M., Hata H., Watanabe M., Komatsu T., Nawasani T., Oyama M., Hata H., Watanabe M., Komatsu T., Nawasani T., Oyama M., Hata H., Watanabe M., Komatsu T., Nawasani T., Oyama M., Hata H., Watanabe M., Komatsu T., Nawashita R., Nakailma Y., Nawamura Y., Okumura K., Nasashi T., Oomplete sequencing and characterization of 11,243 full-length human R., Connelete Sequencing and characterization of 121,243 full-length human R.
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EMBL; AK027379; BAB55072.1; -
PIR; S21205; S21205.
HSSP; P01876; 10W0.
InterPro; IPR007110; Ig-like.
InterPro; IPR003597; Ig_c1.
InterPro; IPR003505; Ig_wHC.
InterPro; IPR033505; Ig_v.
Pfam; PF07654; C1-set; Z.
SWART; SW00406; IGV; 1.
PROSITE; PS00235; IG_MHC; UNKNOWN 1.
PROSITE; PS00230; IG_MHC; UNKNOWN 1.
SEQUENCE 494 AA; 53088 MW; 9AID7AEB5ABE4COB CRC64;
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84.8%; Pred. No. 4.1e-125;
ive 26; Mismatches 41; Indels
PubMed=14702039; DOI=10.1038/ng1285;
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Best Local Similarity 84.8'
Matches 417; Conservative
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423 RQEPSQGTTTFAVTSILRVAAEDWKKGDTFSCMVGHEALPLAFTQKTIDRLAGKPTHVNV 482
417
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      140 LDP-----WGQGTLVTVSSASPTSPKVFPLSLCSTQPDGNVVIACLVQGFFPQEPLSVTWS 195
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                                 363 SGNTFRPEVHLLPPPSEELALNELVTLTCLARGFSPKDVLVRWLQGSQELPREKYLTWAS
                                                                                                                      RQEPSQGTTTFAVTSILRVAAEDWKKGDTFSCMVGHEALPLAFTQKTIDRLAGKPTHVNV
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Robo G., Han M., Wiemann S.;
Robo G., Han M., Wiemann S.;
Robo G., Han M., Wiemann S.;
Runterd (Aug.2003) to the EMBL/GenBank/DDBJ databases.
R HSSP; P01751; 1A6W.
R InterPro; IPR001599; 1G.
R InterPro; IPR001599; 1G.
R InterPro; IPR001599; 1G.
R InterPro; IPR001596; 1g_MHC.
R InterPro; IPR001596; 1g_MHC.
R R ROPOSTS; SMO0409; 1G.1.
R SMART; SMO0409; 1G.1.
R SMART; SMO0406; 1Gv; 1.
R R ROSITE; PS50815; 1G_LIKE; 4.
R PROSITE; PS50815; 1G_LIKE; 4.
R PROSITE; PS508290; 1G_MHC; UNKNOWN_1.
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Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                05-JUL-2004 (TrEMBLrel. 27, Created)
05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
Hypothetical protein DKFZp686G21220 (Fragment).
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85.5%; Pred. No. 7.3e-125;
iive 17; Mismatches 44;
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The German Human cDNA Consortium;
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Krausberg R.L., Feingold E.A., Grouse L.H., Derge J.G., Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G., Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G., Altachul S.F., Zeeberg B., Buetow. K.H., Schaefer C.F., Bhar N.K., Altschul S.F., Zeeberg B., Buetow. K.H., Schaefer C.F., Bhar N.K., Altschul S.F., Jordan H., Moore T., Max S.I., Wang J., Hesteh F., Stapleron M., Soares M.B., Bonaldo M.F., Casavant T.L., Schetz T.E., Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C., Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J., Abramson R.D., Mullahy S.J., Nackernan K.J., Malek J.A., Gunaranne P.H., Machay B.J., McKernan K.J., Lu X., Gibbs R.A., Atlahon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A., Faby J., Helton E., Ketteman M., Madan A., Kodrigues S., Sanchez A., Millahon D.K., Muzny D.M., Sodergren E.D., Dickson M.C., Abreshy M., Touchman J.W., Gareen E.D., Dickson M.C., An Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C., A Rating M.J., Matra M.J., Smailus D.E., Schnerch A., Schein J.E., Jones S.J., Matra M.A., In M., Smailus D.E., Schnerch A., Schein J.E., Tand Mouse C.D., Shall Marka M.A., Shallaka D., Schmutz J., Myers R.M., Butterfield Y.S., Generation and initial analysis of more than 15,000 full-length human mouse CDMA seedences.
                                                                                                                                                                                                                  336 YSVSSVLPGCAEPWNHGKTFTCTAAYPESKTPLTATLSKSGNTFRPEVHLLPPPSEELAL 395
                                                                                                                                                                                                                                                                                                     NELVTLTCLARGFSPKDVLVRWLQGSQELPREKYLTWASRQEPSQGTTTFAVTSILRVAA 438
216 LYTTSSQLTLPATQCLAGKSVTCHVKHYTNPSQDVTVPCPVPSTPPTPSPSTPPTPSPSC 275
                                                                                         CHPRISTHRPALEDLILGSEANLTCTLTGLRDASGVTFTWTPSSGKSAVQGPPERDLCGC 335
                                                                                                                                                                                  YSVSSVLSGCAEPWNHGKTFTCTAAYPESKTPLTATLSKSGNTFRPEVHLLPPPSEELAL 378
                                                                                                                                                                                                                                                                                                                                            396 NELVTLTCLARGESPKDVLVRWLQGSQELPREKYLTWASRQEPSQGTTTFAVTSILRVAA 455
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
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Strausberg R.;

Strausberg R.;

Submitted (JUN-2004) to the EMBL/GenBank/DDBJ databases.

EMBL; BC073771; AA473771.1; -.

InterPro; IPR003599; IG.

InterPro; IPR003599; IG.

R InterPro; IPR003599; IG.

R InterPro; IPR003596; Ig-V.

R InterPro; IPR003596; Ig-V.

R Pfam; PF00047; IG; 3.

R SMART; SM00409; IG; 4.

R SMART; SM00409; IG; 1.

R SMART; SM00406; IGV; 1.

R SMART; SM00406; IGV; 1.

R PROSITE; PS00290; IG_LIKE; 4.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        QGGMX2 PRELIMINARY; PRT; 493 AA. QGGMX2; 05-JUL-2004 (TrEMBLrel. 27, Created) 05-JUL-2004 (TrEMBLrel. 27, Last sequence update) 05-JUL-2004 (TrEMBLrel. 27, Last annotation update) Hypothetical protein. Homo sapiens (Human).
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                         418
                                                                                                                                                                                                                                                                        QEPSQGTTTFAVTSILRVAAEDWKKGDTFSCMVGHEALPLAFTQKTIDRLAGKPTHVNVS 478
                                                                                                                                                                                                                                                                                                     81 YAQKFQGRVTITADESTSTAYMELSSLRSEDTAVYYCA--RDPFLHYWGQGTLVTVSTAS 138
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SHYFRPRLTVTRDASANTVYMELTSLTSEDTAVYFCASERGGLFDVWGPGTTVTVSSAS 155
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                                                                                                                                               GNTFRPEVHLLPPPSEELALNELVTLTCLARGFSPKDVLVRWLQGSQELPREKYLTWASR
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Bloecker H., Boecher M., Mewes H.W., Weil B., Amid C., Osanger A., Frobo G., Han M., Wiemann S.; Submitted (AuG-2003) to the EMBL/GenBank/DDBJ databases. EMBL; BX640847; CAR45917.1; --
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Homo sapiens (Human).
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
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88.3%; Pred. No. 9.7e-125;
ive 18; Mismatches 35; Indels
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05-JUL_2004 (TrEMBLrel. 27, Last sequence update)
05-JUL_2004 (TrEMBLrel. 27, Last annotation update)
Hypothetical protein DKFZp686J11235 (Fragment).
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Interpro; IPR001109; Ig-like.
Interpro; IPR001109; Ig-like.
Interpro; IPR001597; Ig_c1.
Interpro; IPR001596; Ig_wHC.
Interpro; IPR001596; Ig_wHC.
Interpro; IPR001596; Ig_wY.
INTERPRO; IRR010109; IG_WHC.
INTERPRO; IRR010109; IG_WHC.
INTERPRO; IRR010109; IG_WHC; IRRE; IRR010109; IG_WHC; IRRE; IRR010109; IG_WHC; IRRE; IRR010109; IG_WHC; UNKNOWN_I.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A.
TISSUE=Human small intestine;
The German Human cDNA Consortium;
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Matches 416; Conservative
                                                                                                                                                                                                                                                                                                                                                                                        PRELIMINARY;
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                                                                                                                                     65 GLEWMGGIIPIFGTANYAQKFQGRVTITADESTSTAYMELSSLRSEDTAVYYCARD--- 120
                                                                                                                                                                                                                                                                                            VPSTPPTPSPSTPPTPSPSCCHPRLSLHRPALEDLLLGSEANLTCTLTGLRDASGVTFTW 298
                                                                                                                                                                                                                                                                                                                                             299 TPSSGKSAVQGPPDRDLCGCYSVSSVLSGCAEPWNHGKTFTCTAAYPESKTPLTATLSKS 358
                                                                                                   64
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R EMBL, AKO74651; BAC11114.1; -.. R RSP; PO1876; 10W0.

R InterPro; IPR001010; Ig-like.

R InterPro; IPR003006; Ig-MHC.

R InterPro; IPR003596; Ig-MC.

R InterPro; IPR003596; Ig-W.

R Pfam; PF07654; Cl-Set; Z.
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                                                                                                                                                                                                                                                                                                                                                                                                             363 GNTFRPEVHLLPPPSEELALNELVTLTCLARGFSPKDVLVRWLQGSQELPREKYLTWASR
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                                                                                      5 GFLWALVISTCLEFSMAQVQLVQSGAEVKKPGSSVRVSCKASGGTFSSYAISWVRQAPGQ
                                                                                                                                                                                        121 -- PFLHYWGQGTLVTVSTASPTSPKVFPLSLCSTQPDGNVVIACLVQGFFPQEPLSVTWS
                                                                                                                                                                                                                                          ESGOGVTARNFPPSQDASGDLYTTSSQLTLPATQCLAGKSVTCHVKHYTNPSQDVTVPCP
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                                                               Gaps
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                            7;
                                     2; Length 493;
                                  Query Match
84.4%; Score 2204.5; DB 2; Length
Best Local Similarity 84.5%; Pred. No. 1.8e-124;
Matches 415; Conservative 26; Mismatches 43; Indels
l protein.
493 AA; 52865 MW; 558999305B286203 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              01-OCT-2002 (TrEMBLrel. 22, Created)
01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
Hypothetical protein FLJ90170.
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Hypothetical
SEQUENCE 49
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                                                                                                                                                                      Gaps
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EMBL; BX640624; CAE45778.1; -. HSSP; P01842; 1AQK.
InterPro; IPR001599; Ig.
InterPro; IPR001597; Ig.-1ike.
InterPro; IPR001597; Ig.-1ike.
InterPro; IPR001596; Ig.-WHC.
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
NCBI_TaxID=9606;
                                                                                                                                                                 6
                                                                                                           84.3%; Score 2201.5; DB 2; Length 84.8%; Pred. No. 2.7e-124; ive 23; Mismatches 43; Indels
PS50815; IG_LIKE; 4.
PS00290; IG_MHC; UNKNOWN 1.
493 AA; 53224 MW; 12ECD7E094777101 CRC64;
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05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
Hypothetical protein DKFZp686K18196 (Fragment)
Name-DKFZp686K18196;
Homo sapiens (Human)
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TISSUE=Human esophagus tumor;
The German Human cDNA Consortium;
                                                                                                                                                                 Matches 417; Conservative
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WMGGIIPIFGTANYAQKFQGRVTITADESTSTAYMELSSLRSEDTAVYYCARDPF---- 122
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           126 WSFDLWGRGTLVSVSSASPTSPKVFPLSLCSTQPDGNVVIACLVQGFFPQEPLSVTWSES 185
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         246 STPPTPSPSTPPTPSPSCCHPRLSLHRPALEDLLLGSEANLTCTLTGLRDASGVTFTWTP 305
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      301 SSGKSAVQGPPDRDLCGCYSVSSVLSGCAEPWNHGKTFTCTAAYPESKTPLTATLSKSGN 360
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        366 TFRPEVHLLPPPSEELALNELVTLTCLARGFSPKDVLVRWLQGSQELPREKYLTWASRQE 425
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               8 WALVISTCLEFSMAQVQLVQSGAEVKKPGSSVRVSCKASGGTFSSYAISWVRQAPGQGLE 67
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                123 --LHYWGQGTLVTVSTASPTSPKVFPLSLCSTQPDGNVVIACLVQGFFPQEPLSVTWSES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   181 GQGVTARNFPPSQDASGDLYTTSSQLTLPATQCLAGKSVTCHVKHYTNPSQDVTVPCPVP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STPPTPSPSTPPTPSPSCCHPRLSLHRPALEDLLLGSEANLTCTLTGLRDASGVTFTWTP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TFRPEVHILDPPSEELALNELVTLTCLARGFSPKDVLVRWLQGSQELPREKYLTWASRQE
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096KX8;
01-DEC-2001 (TrEMBLrel. 19, Created)
01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
Homo sapiens (Human).
Homo sapiens (Human).
Eukaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length 494;
                                                                                                                 InterPro; 1PR00110; Ig-like.
InterPro; 1PR00110; Ig-like.
InterPro; 1PR003599; Ig.
InterPro; 1PR003006; Ig-MrC.
InterPro; 1PR003596; Ig-WrC.
InterPro; 1PR003596; Ig-WrC.
InterPro; 1PR00407; Ig-I.
InterPro; IRM00409; IG-I.
InterPro; IRM00409; IG-I.
InterPro; IRMN I IG-I:
IRMN
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                    the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          83.9%; Score 2191; DB 2; 184.3%; Pred. No. 1.1e-123; ive 26; Mismatches 43;
                                                EMBL; AK123546; BAC85641.1;
HSSP; P01842; 1AQK.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Local Similarity 84.33
les 412; Conservative
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0965X8
1D 096XX
AC 096XX
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GLEWMGGIIPIFGTAN--YAQKFQGRVTITADESTSTAYMELSSLRSEDTAVYYCA---- 118
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            295 TFTWTPSSGKSAVQGPPDRDLCGCYSVSSVLSGCAEPWNHGKTFTCTAAYPESKTPLTAT 354
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     28 GLSWVFLVA-LLRGVQCQVHLVESGGGVVQPGRSLRLSCAAFGFTFGDHSWHWVRQAPGR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           265 VPCPVPSTPPTPSPSTPPTPSPSCCHPRLSLHRPALEDLLLGSEANLTCTLTGLRDASGV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               445 WASROEPSQCTTTFAVISILRVAAEDWKKGDTFSCRVGHEALPLAFTQKTIDRLAGKPTH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GFLWALVISTCLEFSMAQVQLVQSGAEVKKPGSSVRVSCKASGGTFSSYAISWVRQAPGQ
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                            13; Gaps
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                                                                                                                                                                                                                                                                                                                                                                                           Query Match

84.1%; Score 2196.5; DB 2; Length 519;
Best Local Similarity 84.2%; Pred. No. 5.6e-124;
Matches 417; Conservative 21; Mismatches 44; Indels 13;
Pfam; PF00047; ig; 1.
SMART; SM00409; IG; 4.
SMART; SM00406; IGC1, 2.
SMART; SM00406; IGC1, 2.
PROSITE; PS50835; IG_LIKE; 4.
PROSITE; PS00290; IG_MHC; UNKNOWN_1.
Hypothetical protein.
NOW TER 1
SEQUENCE 519 AA; 56423 MW; F839EE7F811EB88D CRC64;
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05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
Hypothetical protein FLJ41552.
Homo sapiens (Human)
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TISSUE=Colon;
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SEQUENCE FROM N.A. TISSUE=Lung;

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A Straubberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,

Alachner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,

Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,

Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,

A popkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,

A papleron M., Soarse M.B., Bonaldon M.F., Carannori P.L., Scheetz T.E.,

Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,

A Brownstein M.J., Usdin T.B., Toohhyuki S., Carninci P., Prange C.,

Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,

A Boak S.A., McEwan P.J., McKernan K.J., Make J.A., Gubbs R.A.,

A Wilalon D.K., Muzny D.M., Sodergren B.J., Lu X., Gibbs R.A.,

Richards S., Worley K.C., Hale S., Garcia A.M., Gabbs R.A.,

Richards S., Worley K.C., Hale S., Garcia A.M., Gabbs R.A.,

Richards S., Worley A.C., Shevchenko Y., Bouffaus G.G.,

Mhiting M., Madan A., Young A.C., Shevchenko Y., Bouffaus G.G.,

A Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butcerfield Y.S.,

A Jones S.J., Marra M.A.,

T "Generation and initial analysis of more than 15,000 full-length human
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               63
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    4 LWFFLLLVAAPRWVLSQLQLQESGPGLVKSSETLSLTCTVSGGSISSSSYYWGWIRQPPG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    183 TWSESGQGVTARNFPPSQDASGDLYTTSSQLTLPATQCLAGKSVTCHVKHYTNPSQDVTV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PCPVPSTPPTPSPSTPPTPSPSCCHPRLSLHRPALEDLLLGSEANLTCTLTGLRDASGVT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        243 PCPVPSTPPTPSPSTPPTPSPSCCHPRLSLHRPALEDLLLGGSEANLTCTLTGLRDASGVT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             303 FTWTPSSGKSAVQGPPERDLCGCYSVSSVLPGCAEPWNHGKTFTCTAAYPESKTPLTATL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             363 SKGGNTFRPEVHLLPPPSEELALNELVTLTCLARGFSPKDVLVRWLQGSQELPREKYLTW
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ASRQEPSQCTTTFAVTSILRVAAEDWKKGDTFSCMVGHEALPLAFTQKTIDRLAGKPTHV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       64 QGLEWMGGIIPIFGTANYAQKFQGRVTITADESTSTAYMELSSLRSEDTAVYYCARDPF-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               -----LHYWGQGTLVTVSTASPTSPKVFPLSLCSTQPDGNVVIACLVQGFFPQEPLSV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TWSESGOGVTARNFPPSQDASGDLYTTSSQLTLPATQCLAGKSVTCHVKHYTNPSQDVTV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            FIWIPSSGKSAVQGPPDRDLCGCYSVSSVLSGCAEPWNHGKTFTCTAAYPESKTPLTATL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SKSGNTFRPEVHILLPPPSEELALNELVTLTCLARGFSPKDVLVRWLQGSQELPREKYLTW
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               7 LW-ALVISTCLEFSMAQVQLVQSGAEVKKPGSSVRVSCKASGGTF--SSYAISWVRQAPG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ASRQEPSQGTTTFAVTSILRVAAEDWKKGDTFSCMVGHEALPLAFTQKTIDRLAGKPTHV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         12;
MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length 496;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A Strausbergy R.;

L Submitted (OCT-2001) to the EMBL/GenBank/DDBJ databases.

E EMBL; RC016369; AAH16369.1; -.

R HSSP; P010876; 10W0.

R InterPro; IPR00310; Ig-like.

R InterPro; IPR003306; Ig-MHC.

R InterPro; IPR003596; Ig-V.

R InterPro; IPR003596; Ig-V.

R MSRT; SN00406; IGV.

DR PROSITE; PS50835; IG-LIKE; 4.

DR PROSITE; PS00839; IG-LIKE; 4.

DR PROSITE; PS00839; IG-LIKE; 4.

DR ROSITE; PS00839; IG-LIKE; 4.

DR ROSITE; PS00839; IG-LIKE; 4.

DR ROSITE; PS00839; IG-LIKE; 4.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match 81.6%; Score 2131; DB 2; 1
Best Local Similarity 81.8%; Pred. No. 4.6e-120;
Matches 404; Conservative 29; Mismatches 49;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    and mouse cDNA sequences."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TISSUE=Lung;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    236
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SORR RECENT TO DESCRIPTION OF STREET 
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TISSUB-Glandular pool- thyroid;

X MEDLINE-22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;

X RIAUSDER R.D., Collins F.S., Magner L., Shenmen C.M., Schuler G.D.,

A RIASCHUL S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,

A District R.D., Marusina K., Farmer A.A., Rubin G.M., Hong L.,

A Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,

A Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,

A Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,

A Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,

Brownstein M.J., Usdin T.B., Toshiyuki S., Carninoi P., Parage C.,

Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,

Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,

Richards S., Worley D.M., Sodergren E.J., Lu X., Gibbs R.A.,

Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,

Nitling M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,

Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,

Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,

"Generation and initial analysis of more than 15,000 full-length human

mouse G.DA, Sequences."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      19 SQVQLVQSGAEVKKTGASVKVSCKASGYSISDNYIHWVRQAPGQGLEWMAMIRPQNGGTV 78
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      80
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Eutelt
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Submitted (JAN-2004) to the EMBL/GenBank/DDBJ databases.
EMBL; BC065733; AAH65733.1; -.
HSSP; P01751; 1A6W.
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                                                                                                                                                                                                                                                                                            05-JUL-2004 (TrEMBLrel. 27, Created)
05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002)
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                                                                                                                                                                                                                                       480
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INCEPPO; IPRO03599; IG.
INCEPPO; IPRO03597; IG_C1.
INCEPPO; IPRO03597; IG_C1.
INCEPPO; IPRO03596; IG_W.
INCEPPO; IPRO03596; IG_W.
INCEPPO; IPRO0459; IG_N.
SWART; SWO0409; IG, 4.
SWART; SWO0407; IGC1; 3.
SWART; SWO0407; IGC1; 3.
PROSITE; PS50835; IG_LIKE; 4.
PROSITE; PS002909; IG_LIKE; 4.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TISSUE-Glandular pool- thyroid;
                                   483 NVSVVMAEVDGTCY 496
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Matches 402; Conservative
                                                                                                                                                                                                                                    PRELIMINARY;
NVSVVMAEVDGTCY
                                                                                                                                                                                                                                                                                                                                                                                                 Hypothetical protein. Homo sapiens (Human).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Strausberg R.;
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SEQUENCE 48
476
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                                                                                                                                                                                                                                Q6P089
Q6P089;
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VTVSTASPTSPKVFPLSLCSTQPDGNVVIACLVQGFFPQEPLSVTWSESGQGVTARNFPP 191
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TISSUE=Human rectum tumor;

TISSUE=Human rectum tumor;

THE GERMAN Human CDNA Consortium;

Wambutt R., Heubner D., Mawes H.W., Weil B., Amid C., Osanger A.,

Pobo G., Han M., Wiemann S.;

L. Submitted (AUG-2003) to the EMBL/GenBank/DDBJ databases.

R. REMBL; BR0001519; Ig-1ike.

R. InterPro; IPR001599; Ig-1ike.

R. InterPro; IPR001509; Ig-MHC.

R. InterPro; IPR001509; Ig-W.

R. R. InterPro; IPR001509; IG-W.

R. SMART; SM00409; IG; 4.

SMART; SM00406; IG-W.

R. SMART; SM00406; IG-W.

R. SMART; SM00406; IG-W.

R. SMART; SM00406; IG-W.

R. PROSITE; PS06835; IG-MIKE; 4.

R. PROSITE; PS06835; IG-MIKE; UNKNOWN_2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              441 SILRVAAEDWKKGETFSCMVGHEALPLAFTQKTIDRMAGKPTHINVSVVMAEADGTCY
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
NCBI_TaxID=9606;
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05-JUL-2004 (TrEMBLrel. 27, Created)
05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
Name-DrYzD686C02220;
Name-DrYzD68GC02220;
Homo sapiens (Human)
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Matches 395; Conservative
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Trisuper Human rectum tumor;

Trisuper Human cDNA Consortium;

A Poustka A. Albert R., Moosmayer P., Schupp I., Wellenreuther R.,

A Mewes H.W., Weil B., Amid C., Osanger A., Pobo G., Han M., Wiemann S.;

Bubitted (Aug-2003) to the EMBL/GenBank/DDBJ databases.

B Submitted (Aug-2003) to the EMBL/GenBank/DDBJ databases.

R HSSP; P01751; 1A6W.

R HSSP; P01751; 1A6W.

R InterPro; IPR003599; Ig.

R InterPro; IPR003599; Ig.

R InterPro; IPR003595; Ig.

R InterPro; IPR003595; Ig.

R InterPro; IPR003595; Ig.

R InterPro; IPR003595; Ig.

R SWART; SW00409; IG.4.

B SWART; SW00409; IG.4.

R SWART; SW00409; IG.

R SWART; SW00409; IG.

R PROSITE; PS00290; IG.

R PROSITE
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Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
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82.6%; Pred. No. 1.7e-117;
ive 27; Mismatches 34; Indels
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05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
Hypothetical protein DKFZp686016217 (Fragment).
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Search completed: October 25, 2005, 11:07:52 Job time : 73.272 secs

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GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.
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OM protein - protein search, using sw model

Run on:

October 25, 2005, 10:59:42 ; Search time 16.842 Seconds (without alignments) 2793.604 Million cell updates/sec

US-10-644-256-3 '2611 1 MACPGFLWALVISTCLEFSM......GKPTHVNVSVVMAEVDGTCY 489 Title: Perfect score: 'Sequence:

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

283416 segs, 96216763 residues Searched:

283416 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Database :

PIR 79:*
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

1889 72.3 353 1 1889 72.3 353 1 1693.5 64.9 340 2 1656.5 64.9 340 2 11112.5 64.9 342 2 11112.5 48.9 342 2 11113.5 42.6 344 2 1015.5 40.8 344 1 1025.5 39.7 357 2 1025.5 39.7 357 2 1002.5 38.9 358 2 980 37.8 338 2 950 36.3 338 2 883.2 338 2 950 36.4 358 2 883.2 38.3 338 2 883.2 388.3 338 3 883.2 388.3 388 3 883.2 388 3 884.2 388 3 885.2 388 3 885.2 388 3 885.2 388 3 886.2 388 3 886.2 388 3	Result No.	9700	% Query Match	Length	DB	SUMMARIES	Description
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9 1066.5 40.8 344 1 AHMS 1015.5 39.7 357 2 8092 2 1016 38.9 357 2 8092 2 1016 38.9 357 2 8092 2 1016 38.9 357 2 8092 2 1016 38.9 357 2 8092 2 1016 38.9 357 2 8092 2 1016 38.9 357 2 8092 2 1016 38.9 35.0 3 34.0 35.0 3 34.0 35.0 3 34.0 35.0 3 34.0 35.0 3 34.0 3 35.0 3 34.0 3 35.0 3 34.0 3 35.0 3 34.0 3 35.0 3 35.0 3 34.0 3 35.0 3 3	œ	1	2	4	~	596	g alpha
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5 984 37.7 347 2 8092 6 980 37.5 348 2 8092 8 970.5 37.3 348 2 8092 9 959.5 36.7 343 2 8092 9 959.5 36.4 352 2 8092 1 949 36.1 358 2 8092 2 883.5 33.8 33.8 2 8092 4 842 32.2 885 2 A465 5 754 28.9 1 AHRB 7 74 28.9 46 2 83774 8 736.5 28.5 446 2 83734	7	986	7	S	7		g alpha cha
6 980 37.5 348 2 5092 37.3 348 2 5092 37.3 348 2 5092 37.3 348 2 5092 37.3 348 2 5092 37.3 348 2 5092 37.3 348 2 5092 37.4 3 28.5 2 5092 37.4 2 8.6 46 2 5.374 37.5 58.5 5.374 3 58.5 5.5 5.5 5.5 5.5 5.5 5.5 5.5 5.5 5.	'n	984	7	4	7		g alpha
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7 748 28.6 469 2 S3748 8 743 28.5 475 2 S0132 9 736.5 28.2 446 2 S4029	9	754	æ	σ	~	9	g mu chain
8 743 28.5 475 2 SO132 9 736.5 28.2 446 2 S4029	7	748	æ	9	~	8	Ig gamma-2a chain
9 736,5 28,2 446 2 54029	8	743	æ	7	~	2	g gamma-2b
	6	r	ø	4	7	õ	g gamma-2a

Ig gamma-2b chain	Ig heavy chain pre	Ig alpha chain C r	Ig heavy chain pre	Ig Y heavy chain (Ig heavy chain - n	monoclonal antibod	Ig epsilon chain C	Ig gamma-1 chain -	Ig alpha chain - o	Ig mu chain precur	Ig delta chain (WI	Ig heavy chain pre	Ig heavy chain V r	Ig heavy chain V-1	Ig heavy chain V r	
G2MS11	S04845	803298	S22080	B46529	150731	PC4436	S38864	S31459	161901	S12838	S17597	A34891	PH0962	A33548	PH0959	
7	N	N	N	~	7	ď	N	~	7	7	7	~	N	~	0	
474	549	145	470	572	577	444	548	472	132	573	509	568	120	129	116	
28.1	27.7	27.2	26.7	26.6	25.2	24.9	24.2	23.7	23.7	23.3	23.0	21.3	21.2	21.1	20.9	
733.5	723	710.5	697	694	629	651	631	620	619	608	600.5	555.5	552.5	550	544.5	
30	31	35	33	34	32	36	37	38	39	40	41	42	43	44	45	

ALIGNMENTS

	PESTIT. 7
	Ig-alpha-1 chain C region - human
	C; Species: Homo sapiens (man)
	C;bate: 22-may-1981 #Bequence_revision 03-Oct-1995 #text_cnange_0y-Jui-2004 C;Accession: A22360; A92249; A91662; S38979; B53110; A02171
	R.Flangdan, J.G.; Lefranc, M.P.; Rabbitts, T.H.
	Cell. 3), vol2080, 129. Afitle: Mechanisms of divergence and convergence of the human immunoglobulin alpha-1 and Afitle: Mechanisms of divergence and convergence of the human immunoglobulin alpha-1 and
	A,Accesion: A22360
	A MOLECULE VYĐE: UNA A:Pesidines: 1-157 < FFL»
	A.Cross-references: UNIPROT:P01876
	R;Putnam, P.W.; Liu, Y.S.V.; Low, T.L.K.
	A,Title: Pitnary Eructure of a human 1941 ımmunoglobulın. IV. Streptococcai igal proteak A.Reference number: A02049. MITD-7914(016: PMID:107164
	A; Contents: myeloma protein Bur; disulfide bonds
	A;Accession: A92249
	A Wolecule type: protein
	Ajkesidues; 1-16,'26',18', 18',20',18',22'-34',0',,36-45',2',4'-51',6',53-56', 26',59'-01',6',59'-01',70',30',
	D.O.S. b. VOJ-1-4-0. V. A.O.S. D.O.S. b. VOTe. This is the firs] cane in a series
	A.Note: amidation states of residues 178, 197, 238, 239, 244, 287, and 318 were take
	A, Title: The primary structure of a monoclonal 1gA-immunoglobulin (1gA Tro.), II: the ami
	Ajkererence number: Ayloba; Mulu:/60k3/kal; Pmiu:80y331 A.bacasainn. Agika
, -	A. Molecule type: protein
	A, Residues: 1-16, Z', 18, 'B', 20, 'B', 22-34, 'Q', 36-45, 'Z', 47-51, 'B', 53-56, 'ZB', 59-61, 'B', 63-
	,'R',232-237,'QQ',240-243,'Q',245-283,'Q',285-289,'E',291-303,'B',305-353 <kra></kra>
	A) Experimental source: myeloma protein Tro
_	Kirallgreen-debaler, b.; debaler, b.; debaler, w.; bastlan, k.; Kratzin, h.D.; billert, h.; Zimmerman Riol, Chem. Honne-Revler 174, 1023-1028, 1993
_	A; Title: The coralent linkage of secretory component to IgA. Structure of sIgA.
	A; Reference number: \$38978; WUID: 94121784; PMID: 8292260
	A. Accession: S38979
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	R; Yang, C.Y., Kratzin, H.; Gotz, H.; Hilschmann, N.
	Hoppe-Seyler's Z. Physiol. Chem. 360, 1919-1940, 1979
	A;Title: Die Primaerstruktur eines monokionalen 1g41-Immunglobulins (Myelomprotein Tro).
	A.Contentus: annotation; Tro, disulfide bonds
•	
	R;Calero, M.; Bscribano, J.; Grubb, A.; Mendez, E. J. Biol Chem 560 184-189 1994
	Arritle: Location of a novel type of interpolypeptide chain linkage in the human protein
	A;Reference number: A53110; MUID:94103241; PMID:7506257
_	A;Accession: B53110

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Gaps

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257

317 180 437

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C;Species: Homo sapiens (man)
C;Date: 28-Dec-1987 #sequence_revision 28-Dec-1987 #text_change 09-Jul-2004
C;Date: 28-Dec-1987 #sequence_revision 28-Dec-1987 #text_change 09-Jul-2004
C;Accession: B23360
R;Flanagan, J.G.; Lefranc, M.P.; Rabbitts, T.H.
Cell 36, 681-688 1984
A;Filte: Mechanisms of divergence and convergence of the human immunoglobulin alpha-1 and A;Reference number: A94653; MUID:84130179; PMID:6421489
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                                                                                                                                                                                                                                                                                                                                                                                CYSVSSVLSGCAEPWNHGKTFTCTAAYPESKTPLTATLSKSGNTFRPEVHLLPPPSEELA 377
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          241 INELVTLTCLARGFSPKDVLVRWLQGSQELPREKYLTWASRQEPSQGTTTFAVTSILRVA 300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         257 SCCHPRLSLHRPALEDLLLGSEANLTCTLTGLRDASGVTFTWTPSSGKSAVQGPPDRDLC 316
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DLYTTSSQLTLPATQCLAGKSVTCHVKHYTNPSQDVTVPCPVPSTPPTPSPSPSPSPSPSPSPS
                                                                                                                                                                                                                                                                                                                                                                                                         181 CYSVSSVLPGCAEPWNHGKTFTCTAAYPESKTPLTATLSKSGNMFRPEVHLLPPPSEELA
                                                                                                                                                                                                                            61 GDLYTTSSQLTLPATQCPDGKSVTCHVKHYTNPSQDVTVPCPVP------PPP
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                                                                                                               SPTSPKVFPLSLCSTQPDGNVVIACLVQGFFPQEPLSVTWSESGQGVTARNFPPSQDASG
                                                                                                                                          1 SPTSPKVFPLSLCSTQPDGDVVVACLVQGFFPQEPLSVTWSESGQGVTARNFPPSQDASG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                        LNELVTLTCLARGFSPKDVLVRWLQGSQELPREKYLTWASRQEPSQGTTTFAVTSILRVA
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                       Length 352
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A;Cross-references: GDB:119333; OMIM:147000
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A;Introns: 1,1 103/1; 210/1
C;Superfamily: immunoglobulin C region; immunoglobulin homology C;Reywords: immunoglobulin
F;230-302/Domain: immunoglobulin homology <IMM>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 12; Indels
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                       DB 2;
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65.5%; Score 1710.5; DB 3
Best Local Similarity 90.9%; Pred. No. 1.5e-84;
Matches 321; Conservative 7; Mismatches 12.
                    Score 1838; DB 2;
Pred. No. 2.4e-91;
4; Mismatches 7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Ig alpha-2 chain C region (allotype A2m(1)) - human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A;Molecule type: DNA
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Matches 341; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          137 ASPTSPKVFPLSLCSTQPDGNVVIACLVQGFFPQEPLSVTWSESGQGVTARNFPPSQDAS 196
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               317 GCYSVSSVLSGCAEPWNHGKTFTCTAAYPESKTPLTATLSKSGNTFRPEVHLLPPPSEEL 376
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R. Kawamura, S.; Omoto, K.; Ueda, S.
Nuclei Acida Rea. 17, 6732, 1989

A.Title: Nucleotide sequence of the gorilla immunoglobulin alpha 1 gene.
A; Reference number: 505500, MUID:89386006; PMID:2506527

A; Recession: 505500

A; Status: translation not shown
A; Molecule type: DNA
A; Residues: 1-352 < kAM>
A; Cross-references: EMBL:X15045; NID:922900; PIDN:CAA33147.1; PID:922901
C; Genetics: A; Introns: 102/1; 222/1
C; Superfamily: immunoglobulin C region; immunoglobulin homology
C; Keywords: immunoglobulin
F; 242-314/Domain: immunoglobulin homology < IMM>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Ig alpha-1 chain C region - gorilla (fragment)
C;Species: Gorilla gorilla (gorilla)
C;Date: 07-Jun-1990 #sequence_revision 07-Jun-1990 #text_change 23-Jul-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 ASPTSFKVFPLSLCSTQPDGNVVIACLVQGFFPQBPLSVTWSESGQGVTARNFPPSQDAS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  197 GDLYTTSSQLTLPATQCLAGKSVTCHVKHYTNPSQDVTVPCPVPSTPPTPSPFTPSP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       257 SCCHPRLSLHRPALEDLLLGSEANLTCTLTGLRDASGVTFTWTPSSGKSAVQGPPDRDLC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 241 ALNELVILICLARGFSPKDVLVRWLOGSOELPREKYLTWASROEPSOGITIFAVISILRV
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AAEDWKKGDTFSCAVGHEALPLAFTQKTIDRLAGKPTHVNVSVVMAEVDGTCY 353
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 1889; DB 1; Length 353;
Pred. No. 4.7e-94;
1; Mismatches 1; Indels
                                                              A,Gene: GDB:IGHA1
A,Cross-references: GDB:119332; OMIM:146900
Molecule type: protein
Residues: 346-351,'X',353 <CAL>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
Best Local Similarity 99.4%;
Matches 351; Conservative
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9

Gaps

13;

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Aymap position: 14932.33-14922.33
C;Complex: An immunoglobulin heterotetramer subunit consists of two identical light (kapp hain disulfide bonds. In some cases, such as IgA and IgM, the subunits associate into lan C;Superfamily: immunoglobulin c region; immunoglobulin homology cypuscial immunoglobulin homology cipuscial interchain (to alpha chain in another subunit) #status predicted F;339/Disulfide bonds: interchain (to alpha chain in another subunit) #status predicted F;339/Disulfide bonds: interchain (to alpha chain in another subunit) #status predicted
                                                                                                                                                                                                                                                                                   A; Molecule type: protein A; No. 201., P., 103-278, F., 280-295, D., 297-325, VV, 327-334, VV, 336-340 A; Residues: 1-92, P., 94-101, P., 103-278, F., 280-295, D., 297-325, VV, 327-334, VV, 336-340 A; Note: this chain does not form a disulfide bond with the light chain in the A; Note: the Azm(1) allotype appears to be a recombinant chain, being identical (except form a light alpha-1 chain from positions 279 to 340 C; Comment: The Azm(2) allotype sequence of the myeloma protein But is shown.
                                  RiTsuzukida, Y.; Wang, C.C.; Putnam, F.W.
Proc. Natl. Acad. Sci. U.S.A. 76, 1104-1108, 1979
A;Title: Structure of the A2m (1) allotype of human IgA-a recombinant molecule.
A;Reference number: A93829; MUID:79180140; PMID:286295
A;Contents: myeloma protein Lan
A;Accession: A93829
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ig alpha chain C region - pig (fragment)
C;Species: Sus scrofa domestica (domestic pig)
C;Species: Sus scrofa domestica (domestic pig)
C;Accession: 147175
R;Brown, W.R.; Butler, J.E.
MOI. Immunol. 31, 633-642, 1994
A;Pitle: Characterization of a C alpha gene of swine.
A;Reference number: 147175; MUID:94254897; PMID:7545929
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            197 GDLYTTSSQLTLPATQCLAGKSVTCHVKHYTNPSQDVTVPCPVPSTPPTPSPSTPSP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               137 ASPTSPKVFPLSLCSTQPDGNVVIACLVQGFFPQEPLSVTWSESGQGVTARNFPPSQDAS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    63.4%; Score 1656.5; DB 1; Length 340;
85.3%; Pred. No. 1.1e-81;
tive 24; Mismatches 15; Indels 13;
A, Note: the disulfide bond formed by Cys-77 is unaccounted
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A;Status: preliminary: translated from GB/EMBL/DDBJ
A;Molecule type: mRNA
A;Residues: 1-342 <BRO>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A,Gene: GDB:IGHA2
A,Cross-references: GDB:119333; OMIM:147000
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Matches 301; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     C;Genetics:
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Proc. Natl. Acad. Sci. U.S.A. 75, 966-969, 1978

A;Title: Complete amino acid sequence of the alpha2 heavy chain of a human IgA2 immunogl
A;Reference number: A93828; MUID:78137069; PMID:416441
A;Contents: But
A;Accession: A93828
A;Accession: A93828
A;MOLecule type: protein
A;Residues: 1-340 <TOR>
                                                                                                                                                                                                                                                                                                                                                                                                                                                     Ig alpha-2 chain - human (fragment)
(c) Species: Homo sapiens (man)
(c) Species: Homo sapiens (man)
(c) Accession: 156230
(c) Accession: 156230
(d) Accession: 156230
(e) Accession: 156230
(e) Accession: 156230
(f) Access
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        377 ALNELVTLTCLARGFSPKDVLVRWLQGSQELPREKYLTWASRQEPSQGTTTFAVTSILRV 436
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C;Species: Homo sapiens (man)
C;Date: 17-Dec-1982 #sequence revision 17-Dec-1982 #text_change 16-Jul-1999
C;Accesion: A93828, A93829; A02172
R;Torano, A.; Putnam F W
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C;Superfamily: immunoglobulin C region; immunoglobulin homology
F;230-302/Domain: immunoglobulin homology <INM>
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Pred. No. 1.2e-83;
7; Mismatches 14;
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Best Local Similarity 90.4%;
Matches 319; Conservative
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Gispecies: Mus musculus (house mouse)
Cispecies: Musculus (house mouse)
Cispecies: Musculus (house mouse)
Cispecies: Musculus (house)
Cispecies: Mageotte, R.; Sikorav, J.L.; Heidmann, O.; Rougeon, F.
Gene 13, 365-374, 1981
A;Fille: Mouse immunoglobulin A: nucleotide sequence of the structural gene for the alpha
A;Reference number: A94479; MulD:81261947; PMID:6790349
A;Contents: myelomas ABB548 and J558
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Lys, ATG for residue 334
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        121 GFSPKDVLVRWLQGSQELPREKYLTWASRQEPSQGTTTYAVTSILRVAAEDWKKGETFSC 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    254
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  107 PSTICQPSLSLQRPALEDLLIGSDASLTCTLSGLKSTEGVVFTWEPTTGKDAVQKKPVQD 166
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           373
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         167 SCGCFSVSSVLPGCAERWNSGASFTCTVTHPDSETPLTGTIAKVTVNTFPPQVHLVPPPS 226
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              57
                                                                                                                                                                                                                                       Ig alpha chain C region - shrew mouse C;Species: Mus pahari C;Species: Mus pahari C;Species: Mus pahari C;Species: Mus pahari C;Accession: A45966 R;Osborne, B.A.; Golde, T.E.; Schwartz, R.L.; Rudikoff, S. Genetics 119, 925-931, 1988 A;Title: Evolution of the IgA heavy chain gene in the genus Mus. A;Reference number: A45966; MUID:88313645; PMID:2842228 A;Accession: A55966; MUID:88313645; PMID:2842228 A;Accession: preliminary
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            138 SPTSPKVFPLSL---CSTQPDGNVVIACLVQGFFPQEPLSVTWSESGQGVTARNFPPSQD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          2 SPRNPTIYPLTLPPALSSEP---VIIGCLIHDYFPSGTMNVTWGKSGNDITTVNFPPAL-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 195 ASGDLYTTSSQLTLPATQCLAGKSVTCHVKHYTNPSQDVTVPCPVPSTPPTPSPTP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         255 SPSCCHPRLSLHRPALEDLLLGSEANLTCTLTGLRDASGVTFTWTPSSGKSAVQGPPDRD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           LCGCYSVSSVLSGCAEPWNHGKTFTCTAAYPESKTPLTATLSK-SGNTFRPEVHLLPPPS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DB 2; Length 342;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A;Molecule_type: DNA
A;Residues: 1-342 <0SB>
A;Cross-treferences: GBS-113020
A;Note: the authors translated the codon AAC for residue 46 as 1
C;Superfamily: immunoglobulin C region; immunoglobulin homology
C;Keywords: immunoglobulin homology <IMM>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  42.6%; Score 1112.5; DB 2; Length: 58.7%; Pred. No. 1.2e-52; ative 57; Mismatches 71; Indels
                                                                                       MVGHEALPLAFTOKTIDRMAGKPTHINVSVVMAEADGTCY
                                                         MVGHEALPLAFTQKTIDRLAGKPTHVNVSVVMAEVDGTCY
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A, Residues: 1-344 < AUF>
A, Cross references: UNIPROT: P01878
B, Robinson, E.A.; Appella, E.
J. Biol. Chem. 254, 11418-11430, 1979
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Best Local Similarity 58.7%
Matches 209; Conservative
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C'Species: Homo sapiens (man)
C'Date: 28-Dec-1987 #sequence_revision 28-Dec-1987 #text_change 20-Jun-2000
C'Date: 28-Dec-1987 #sequence_revision 28-Dec-1987 #text_change 20-Jun-2000
C'Date: 28-Dec-1987 #sequence_revision 28-Dec-1987 #text_change 20-Jun-2000
R'Flanagan, J.G.; Lefranc, M.P.; Rabbitts, T.H.
Cell 36, 88-68, 1984
A; Flanagan, J.G.; Lefranc, M.P.; Rabbitts, T.H.
A; Reference number: A94653; MUD:84130179; PMID:6421489
A; Reference number: A94653; MUD:84130179; PMID:6421489
A; Residues: 1-220 - FLA>
A; Cross-references: GB:AJ012264; NID:g3819787; PIDN:CAA09968.1; PID:g3819788
C; Comment: This sequence revises entry A2HU (A02172).
A; Genetics:
A; Genetics:
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                                                                                                                                                                                                                                                                                           198 DLYTTSSQLTLPATQCLAGKSVTCHVKHYTNPSQDVTVPCPVPSTPPTPSPSTPPTPSPS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CCHPRLSLHRPALEDLLLGSEANLTCTLTGLRDASGVTFTWTPSSGKSAVQGPPDRDLCG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CYSVSSVLSGCAEPWNHGKTFTCTAAYPESKTPLTATLSK-SGNTFRPEVHLLPPPSEEL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ALNELVILICLARGESPKDVLVRWLQGSQELPREKYLTWASRQEPSQGTTTFAVTSILRV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          230 ALNELVTLTCLVRGFSPKDVLVRWLQGQELPRDKYLVWESLPEPGQAIPTYAVTSVLRV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GFSPKDVLVRWLQGSQELPREKYLTWASRQEPSQGTTTFAVTSILRVAAEDWKKGDTFSC
EMBL:U12594; NID:g555826; PIDN:AAA65943.1; PID:g555827
                                                                                                                                                                                                                                                                138 SPTSPKVFPLSLCSTQPDGNVVIACLVQGFFPQEPLSVTWSESGQGVTARNFPPSQDASG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          270 LEDLLLGSEANLTCTLTGLRDASGVTFTWTPSSGKSAVQGPPDRDLCGCYSVSSVLSGCA
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0
                                                                                                                                                              Length 342;
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                                              A;Gene: IgAcalpha
C;Superfamily: immunoglobulin C region; immunoglobulin homology
F;232-304/Domain: immunoglobulin homology <IMM>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A;Introns: 90/1
C;Superfamily: immunoglobulin C region; immunoglobulin homology
C;Keywords: immunoglobulin
F;il0-182/Domain: immunoglobulin homology <IMM>
                                                                                                                                                        48.9%; Score 1275.5; DB 2; Length
68.8%; Pred. No. 2.4e-61;
Live 32; Mismatches 65; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Ig alpha-2 chain C region (allotype A2m(2)) - human (fragment)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A;Cross-references: GDB:119333; OMIM:147000
A;Map position: 14q32.33-14q32.33
                                                                                                                                                Query Match
Best Local Similarity 68.88
Matches 243; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
Best Local Similarity 93.2'
Matches 205; Conservative
Cross-references:
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C,Accession: S09269
R;Burnett, R.C.; Hanly, W.C.; Zhai, S.K.; Knight, K.L.
R;Burnett, R.C.; Hanly, W.C.; Zhai, S.K.; Knight, K.L.
A;Title: The IgA heavy-chain gene family in rabbit: cloning and sequence analysis of 13
A;Reference number: S09264; MUID:90076124; PMID:2512120
                                                                                                                                                                                                                                                                                                                                       60 SSLYTTCSVLSLPAEQCPAGNSVACRVEH-NNKRQDLTVPCLACNKPIIEPPTKPTCPCP 118
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              61 YTTCSLLRLLAEQCPEENSVACHVEHNYDKGQHVTVPSPPECQPPTPGPSDTTTCPCPCP 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               241 SEELALNELVTLTCLVRGFSPKDVLVYWTNKGVNVPENSFLVWKPLPEPGQEPTTYAVTS 300
                                                                                                                                                                                               140 TSPKVFPLSL--CSTQPDGNVVIA-CLVQGFFPQEPLSVTWSESGOGVTARNFPPSQDAS 196
                                                                                                                                                                                                                                                                                                                                                                                                                                              119 CPSPSCGKPSLSLQRPDLGDLLLDSNASLTCTLRGLLNPEGAVFTWNPTNGKEFVQQSAQ 178
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        RDLCGCYSVSSVLSGCAEPWNHGKTFTCTAAYPE-SKTPLTATLSK-SGNTFRPEVHLLP 370
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PPSEELALNELVTLTCLARGFSPKDVLVRWLQGSQELPREKYLTWASRQEPSQGTTTFAV 430
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              239 PPSEELALALNALVTLTCLVRGFSPKDVLVYWTNKGLQVPKDSFLVWKPLPEPGQEPTTYAV 298
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    140 TSPKVFPLSLCSTQPDGNVVIACLVQGFFPQEPLSVTWSESGQGVTARNFPPSQDASGDL 199
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    255 SPSCCHPRLSLHRPALEDLLLGSEANLTCTLTGLRDASGVTFTWTPSSGKSAVQGPPDRD 314
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          179 RDHCGCYSVSSVLPGCAEPWNAGTVFTCTVTHPEIDSGSLTATISKDTGSLIPPQVHLLP 238
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TSILRVAAEDWKKGDIFSCMVGHEALPLAFIQKTIDRLAGKPTHVNVSVVMAEVDGTCY 489
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    299 TSLIRVPAEDWNQNESYTCVVGHEGLAEHFTQKTIDRLAGKPTHVNVSVVVADVEGVCY 357
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Ig alpha chain C region - rabbit (fragment)
C;Species: Oryctolagus cuniculus (domestic rabbit)
C;Date: 29-Jan-1993 #sequence_revision 29-Jan-1993 #text_change 16-Jul-1999
                                                                                                                                                                                                                             3 TPPIIFPLTCPGCVLKDTSATIVAGCLIRGFFPRGPLGVTWNDNRANLT---FPPVQSAT
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                                                                                                                                                                                                                                                                                                                                                                                                               TPSPSCCHPRLSLHRPALEDLLLGSEANLTCTLTGLRDASGVTFTWTPSSGKSAVQGPPD
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                                                                                                                                                Gaps
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                                                                                              Length 357;
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A; Status: not compared with conceptual translation
A; Molecule type: DNA
A; Residues: 1-357 < BUR>
C; Superfamily: immunoglobulin C region; immunoglobulin homology
C; Keywords: immunoglobulin
F; 142-208/Domain: immunoglobulin homology < IMM>
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39.1%; Score 1022; DB 2; Length 35
Best Local Similarity 56.9%; Pred. No. 8.4e-48;
Matches 203; Conservative 35; Mismatches 109; Indels
                                                                                        Query Match
39.7%; Score 1035.5; DB 2; Length
Best Local Similarity 57.1%; Pred. No. 1.6e-48;
Matches 205; Conservative 43; Mismatches 98; Indels
             C;Keywords: immunoglobulin
F;142-208/Domain: immunoglobulin homology <IMM>
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S09269
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                                                                                                                                                                                                                                                                                                                                                  A;Title: Amino acid sequence of a mouse myeloma immunoglobin heavy chain (MOPC 47A) with A;Reference number: A92245; MUID:80049769; PMID:115869 A;Contents: MOPC 47A
                                                                                                              A; Molecule type: protein
A; Molecule type: protein
A; Mesidues: 1, A', 3-17, 'C', 19-66, 'S', 68-72, 'T', 74-134, 'O', 136-140, 'D', 142-167, 'E', 169-21
A; Mote: Lhe final C-region domain is deleted from this chain
A; Mote: Cys-18 may participate in the heavy-light chain bond
B; Robinson, E.A.; Appella, E.
Proc. Natl. Acad. Sci. U.S.A. 77, 4909-4913, 1980
A; Title: Complete amino acid sequence of a mouse immunoglobulin alpha chain (MOPC 511).
A; Reference number: A93857; MUID:81054880; PMID:6776528
A; Contents: M511
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                13
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             198 DLYTISSQLTLPATQCLAGKSVTCHVKHYTNPSQDVTVPCPVPSTPPTPSPSTPPTPSPS 257
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C;Species: Oryctolagus cuniculus (domestic rabbit)
C;Date: 29-Jan-1993 #sequence_revision 29-Jan-1993 #text_change 16-Jul-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      61 GRYTMSNQLTLPAVECPEGESVKCSVQHDSNPVQELDVNCSGP-TPP-----PPITIPS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    138 SPTSPKVFPLSLCSTQPDGNVVIACLVQGFFPQEPLSVTWSESGQGVTARNFPPSQDASG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  258 CCHPRLSLHRPALEDLLLGSEANLTCTLTGLRDASGVTFTWTPSSGKSAVQGPPDRDLCG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CYSVSSVLSGCAEPWNHGKTFTCTAAYPESKTPLTATLSK-SGNTFRPEVHLLPPPSEEL
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A;Status: not compared with conceptual translation
A;Molecule type: DNA
A;Molecule type: DNA
A;Kesidues: 1-357 < ABUR>
C;Superfamily: immunoglobulin C region; immunoglobulin homology
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R; Burnett, R.C.; Hanly, W.C.; Zhai, S.K.; Knight, K.L.
EMBO J. B. 4041-4047, 1989
A; Title: The 19A heavy-chain gene family in rabbit: cloning
A; Reference number: S09264; MUID:90076124; PMID:2512120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          40.8%; Score 1066.5; DB 58.4%; Pred. No. 3.4e-50; iive 53; Mismatches 83
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  206; Conservative
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Best Local Similarity
Matches 206; Conservat
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124 YSSGWYPNSDYYYYGMDVWGOGTTVTVSSGSASAPTLFPLVSCENSPSDTSSVAVGCLAO 183
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                                                                                                                                                                                                                                                                                                                                                    184 DFLP-DSITFSWKYKNNSDISSTRGFP--SVLRGGKYAATSQVLLPSKDVMQGTDEHVVC 240
                                                                                                                                                                                                                                                                                                                                                                                                                 241 KVQH-PNGNKEKNVPLPVIAELPPKVSVFVPPRDGFFGNPRSKSKLICQATGFSPRQIQV 299
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       257 ----SCCHP-----RLSLHRPALEDLLLGSEANLTCTLTGLRDASGVTFTWTPSSGKS 305
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                                                                               6 FLWALVISTCLEFSMAQVQLVQSGAEVKKPGSSVRVSCKASGGTFSSYAISWVRQAPGQG
                                                                                                   LEWMGGIIPIFGTANYAQKFQGRVTITADESTSTAYMELSSLRSEDTAVYYCAR-----
                                                                                                                                                                                                                                     -----DPFLHY----WGQGTLVTVSTASPTSPKVFPLSLCSTQPD--GNVVIACLVQ
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SGNTFRPEVHLLPPPSEELALNELVTLTCLARGFSPKDVLVRWLQGSQELPREKYLTWAS
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    Length 627;
    DB 2;
Query Match 38.4%; Score 1002.5; DB 2; Best Local Similarity 39.2%; Pred. No. 1.6e-46; Matches 239; Conservative 66; Mismatches 157;
                                                                                                                                                                                                                                                                                                                                                                                           222 HVKHYTNPSQDVTVPCPV-PSTPPTPSPSTPPTP----
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C.Species: Oryctolagus cuniculus (domestic rabbit)
C.Species: Oryctolagus
C.Species: Oryctolagus
C.Species: Oryctolagus
R.Burnett, R.C.; Hanly, W.C.; Zhai, S.K.; Knight, K.L.
EMBO J. 8, 401-4047, 1389
A.Title: The IgA heavy-chain gene family in rabbit: cloning and sequence analysis of 1
A.Reference number: S09264; MUID:90076124; PMID:2512120
A.Reference number: S09264; MUID:90076124; PMID:2512120
A.Reference number: S09265
A.Scatus: not compared with conceptual translation
A.Molecule type: DNA
A.Residues: 1-357 calls
C.Superfamily: immunoglobulin C region; immunoglobulin homology
C.Keywords: immunoglobulin homology <IMM>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        180 HCGCYSVSSVLPGCAVLWNAGTEFTCTVTHPEIEGDSLIGTISKDTGSLIPPQVHLLPPP 239
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     315 LCGCYSVSSVLSGCAEPWNHGKTFTCTAAYPESK-TPLTATLSK-SGNTFRPEVHLLPPP 372
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     4 SSPDLIPLPCPILEPGEPMVIGCLIRGFFPRGPLTVTWNVSGESVI --- FPPVPSPPSSL
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                  ILRVAAEDWKKGDTFSCMVGHEALPLAFTQKTIDRLAGKPTHVNVSVVMAEVDGTCY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        12;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length 357;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match 38.9%; Score 1016; DB 2; Length 3 Best Local Similarity 57.3%; Pred. No. 1.7e-47; Matches 205; Conservative 35; Mismatches 106; Indels
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C.Species: Oryccolagus cuniculus (domestic rabbit)
C.Species: Oryccolagus cuniculus (domestic rabbit)
C.Date: 29-Jan-1993 #sequence_revision 29-Jan-1993 #text_change 16-Jul-1999
C.Sacession: S09268
M. **Riburnett, R.C.; Hanly, W.C.; Zhai, S.K.; Knight, K.L.
EMBO J. 8, 4041-4047, 1989
A;Title: The IgA heavy-chain gene family in rabbit: cloning and sequence analystaces on mumber: S09264; MUID:90076124; PMID:2512120
A;Accession: S09268
A;Accession: S09268
A;Accession: Mulpipe: DNA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              37.8%; Score 986; DB 2; Length 358; ilarity 55.4%; Pred. No. 7e-46; Conservative 41; Mismatches 105; Indels
                                                                                                                                                                                                                                                                                                                                                                         A;Residues: 1-358 <BUR>
C;Superfamily: immunoglobulin C region; immunoglobulin homology C;Keywords: immunoglobulin
F;248-320/Domain: immunoglobulin homology <IMM>
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Ryburnett, R.C.; Hanly, W.C.; Zhai, S.K.; Knight, K.L.
BMBO J. 8, 4041-4047, 1989
A,Title: The IgA heavy-chain gene family in rabbit: cloning and sequence analysis of A,Title: The IgA heavy-chain gene family in rabbit: cloning and sequence analysis of A,Teference number: S09264; MUID:90076124; PMID:2512120
A,Reference number: S09274; PMID:2512120
A,Reference number: S09274
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      292
                                                                                                                                                                                                                                                                                                                                                                                                                                                        61 GPYTTCSLLSLTPEQCPEDDNVVCHVEHNYDKGQNLTVLYP-ECQPPTPSPTTCTCPC 119
                                                                                                                                                                                                                                    120 CPSPSCGEPSLSLQRPDLGDLLLNSNASLTCTLRGLLDPEGAVFTWEPTFGKEPVQLSPK 179
                                                                                                                                                                                                                                                                                                                                                                      112
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         375 ELALNELVILICLARGESPKDVLVRWLQGSQELPREKYLTWASRQEPSQGTTTFAVTSIL 434
                                                                                                                                                                                           253 TPSPSCCHPRISIARPALEDILLGSEANLICTLIGLRDASGVIFTWTPSSGKSAVQGPPD 312
                                                                                                                                                                                                                                                                                                                             313 RDLCGCYSVSSVLSGCAEPWNHGKTFTCTAAYPESK-TPLTATLSK-SGNTFRPEVHLLP 370
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         140 TSPKVFPLSLCSTQPDGN---VVIACLVQGFFPQEPLSVTWSESGQGVTARNFPPSQDAS 196
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SCCHPRISLHRPALEDLILGSEANLTCTLTGLRDASGVTFTWTPSSGKSAVQGPPDRDLC 316
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GCYSVSSVLSGCAEPWNHGKTFTCTAAYPESK-TPLTATLSK-SGNTFRPEVHLLPPPSE 374
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      61
4 SPRLFPLIHPRCALKDTSATVIAGCLIRGFFPLGPLSVSWNASGKNVT---FPPVPSGTS 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Ig alpha chain C region - rabbit (fragment)
C;Species: Oryctolagus cuniculus (domestic rabbit)
C;Date: 29-Jan-1993 #sequence_revision 29-Jan-1993 #text_change 16-Jul-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              233 ELALNALVTLTCLVRGFSPKDVLVSWTNKGVKVPENSFLVWKPLPEPGQDPTTYAVTSLL
                                                                DLYTTSSQLTLPATQCLAGKSVTCHVKHYTNPSQDVTVPCPVPSTPPTPSPSTP----P
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  14; Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       37.7%; Score 984; DB 2; Length 347;
54.4%; Pred. No. 8.6e-46;
tive 45; Mismatches 103; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Search completed: October 25, 2005, 11:08:25 Job time : 18.842 secs
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Best Local Similarity 54.4%
Matches 193; Conservative
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GenCore version (c) 1993 - 2005
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ALIGNMENTS

Abp73848 standard; protein; 497 AA.

AC Abp73848 standard; protein; 497 AA.

AC Abp73848;

AC Abp73848;

AC Abp73848;

AC Abp73848;

AC Abp73848;

Buman anti-HSV antibody HX8 heavy chain (+ mouse leader), SEQ:2.

BE Human anti-HSV antibody HX8; IgA; heavy chain; antibody.

AC Homo sapiens.

Be Horpes simple antibody HX8; IgA; heavy chain; antibody.

AC Homo sapiens.

Be Horpes simple antibody HX8; IgA; heavy chain; antibody.

Chimeric.

Chimeric.

AC Homo sapiens.

AC Horpes HAV1 HY8; HAV2; human; mouse; leader sequence; home sapiens.

Chimeric.

AC Homo sapiens.

AC Horpes HAV2; human; mouse; leader sequence; home sapiens.

AC Horpes HAV2; human; mouse; leader sequence; human sapiens.

AC Horpes HAV2; human; mouse; leader sequence; human sapiens.

AC Horpes HAV2; human; mouse; leader sequence; human sapiens.

AC Horpes HAV2; human; mouse; leader sequence; human sapiens.

AC Horpes HAV2; human; human; human h

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                          The invention relates to the production of immunoglobulins in plants, wherein at least a portion of the glycans attached to the immunoglobulins lack fucose. The immunoglobulins produced can be of any class (i.e., IgG, IgA, IgB or IgD) and is especially an anti-herpes simplex virus (HSV) antibody or an anti-alphaVbeta3, alphaVbeta5 dual integrin cantibody. The invention also relates to constructs, plasmids and vectors for producing the immunoglobulins; transformed plant cells, calli, plant tissues and whole plants for producing the immunoglobulins, the immunoglobulins, methods for producing the immunoglobulins. The immunoglobulins may be use of such immunoglobulins. The immunoglobulins of the invention way be used to treat HSV infection or tumour angiogenesis. The invention contaminants such as viruses and elimination of pathogenic contaminants such as viruses and prions, with a simplified (i.e., non-plant-specific) glycosylation profile which reduces the risk that the immunoglobulin may not be functional in animals. The present sequence immunoglobulin may not be functional in animals. The present sequence represents the human antimates.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ä
                                                                                                                                                                                                                                                                             Novel plant-produced immunoglobulin having glycopeptide or glycan profile with reduced fucosylation, useful for treating herpes simplex virus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        199
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      VIVSTASPISPKVFPLSLCSTQPDGNVVIACLVQGFFPQEPLSVTWSESGQGVTARNFPP 191
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            260 PTPSPSCCHPRLSLHRPALEDLLLGSEANLTCTLTGLRDASGVTFTWTPSSGKSAVQGPP 319
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PSEELALNELVTLTCLARGFSPKDVLVRWLQGSQELPREKYLTWASRQEPSQGTTTPAVT 439
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DRDLCGCYSVSSVLSGCAEPWNHGKTFTCTAAYPESKTPLTATLSKSGNTFRPEVHLLPP 371
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   320 ERDLCGCYSVSSVLPGCAEPWNHGKTFTCTAAYPESKTPLTATLSKSGNTFRPEVHLLPP 379
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PSEELALNELVTLTCLARGFSPKDVLVRWLQGSQELPREKYLTWASRQEPSQGTTTFAVT 431
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         22 QVQLVQSGAEVKKPGSSVRVSCKASGGTFSSYAISWVRQAPGQGLEWMGGIIPIFGTANY
                                                                     Karnoup AL, Anderson WHK;
Taylor D, Roberts JL;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       10; Gaps
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                                                                     Hein MB, Hiatt AC,
I, Rubin-Wilson B,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            HSV1/HSV2 monoclonal IgA antibody HX8
                                                                                                                                                                                                                                                                                                                                                                                                                    Claim 74; SEQ ID NO 2; 212pp; English.
(EPIC-) EPICYTE PHARM INC
                                                                 Glancy T, He
Petolino J,
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                                                                                                                                                                                                        N-PSDB; ADP73847
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                                                                     Briggs K,
Pareddy D,
                                                                                                                                                                                                                                                                                                                                                  infection.
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SILRVAAEDWKKGDTFSCAVGHEALPLAFTQKTIDRLAGKPTHVNVSVVMAEVDGTCY 497

SILRVAAEDWKKGDTFSCMVGHEALPLAFTQKTIDRLAGKPTHVNVSVVMAEVDGTCY

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~ RESULT

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374 SPSCCHPRLSLHRPALEDLLLGSEANLTCTLTGLRDASGVTFTWTPSSGKSAVQGPPERD 433
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 The invention relates to a novel method for producing a polypeptide in a plastid comprising introducing a first recombinant nucleic acid molecule control that the plastid where the first recombinant nucleic acid molecule comprises a first polynucleotide which encodes at least one polypeptide. The method of the invention may be useful for producing polypeptides in chloroplasts, specifically antibodies and antibody chimera that bind tetanus toxin or a herpes simplex virus (HSV). The polynucleotides and polypeptides may useful in producing transgenic plants. The current sequence is that of the chloroplast-codon-optimised HSV8-1sc anti-HSV antibody protein of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Producing polypeptides in chloroplasts, useful in producing antibodies, by introducing a first recombinant nucleic acid molecule comprising a first polynucleotide encoding at least one polypeptide.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         254 SPASPTSPKVFPLSLCSTQPDGNVVIACLVQGFFPQEPLSVTWSESGQGVTARNFPPSQD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                314 ASGDLYTTSSQLTLPATQCLAGKSVTCHVKHYTNPSQDVTVPCPVPSTPPTPP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 134 LEQSGAEVKKPGSSVKVSCKASGGSFSSYAINWVRQAQGGLEWMGGLMPIFGTTNYAQK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SPSCCHPRLSLHRPALEDLLLGSEANLTCTLTGLRDASGVTFTWTPSSGKSAVQGPPDRD
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            25 LVQSGAEVKKPGSSVRVSCKASGGTFSSYAISWVRQAPGQGLEWMGGIIPIFGTANYAQK
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
                                                                                                                                                             plastid; chloroplast; antibody chimera; tetanus toxin;
herpes simplex virus; HSV; transgenic; HSV8-1sc; large single chain.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         10;
                                                                                                                           Chloroplast-codon-optimised HSV8-1sc anti-HSV antibody protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length 630;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     89.4%; Score 2335; DB 7;
92.4%; Pred. No. 6.3e-127;
tive 11; Mismatches 15;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Claim 176; SEQ ID NO 48; 174pp; English
                  ADF69023 standard; protein; 630
                                                                                                                                                                                                                                                                                                                                                                              23-APR-2002; 2002US-0375129P.
19-DEC-2002; 2002US-0434957P.
                                                                                                                                                                                                                                                                                                                                            23-APR-2003; 2003WO-US012997.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           439; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Mayfield SP, Franklin S;
                                                                                                                                                                                                                                                                                                                                                                                                                                    (SCRI ) SCRIPPS RES INST
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      WPI; 2003-865583/80.
N-PSDB; ADF69022.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 630 AA;
                                                                                                                                                                                                                                                                     WO2003091413-A2
                                                                                                                                                                                                                 Unidentified
                                                                                         12-FEB-2004
                                                                                                                                                                                                                                                                                                       06-NOV-2003.
                                                                                                                                                                                                                                      Synthetic
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                                                      ADF69023;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         135
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i K, Irie R, Tamechika I;
Masuho Y;
                                                                              263 SPASPISPKVPPLSLCSTQPDGNVVIACLVQGFFPQEPLSVTWSESGQGVTARNFPPSQD 322
                                                            STASPISPKVPPLSLCSTQPDGNVVIACLVQGFFPQEPLSVTWSESGQGVTARNFPPSQD 194
                                                                                                                                                        323 ASGDLYTTSSQLTLPATQCLAGKSVTCHVKHYTNPSQDVTVPCPVPSTPPTPSPSTPPTP 382
                                                                                                                                                                                                          383 SPSCCHPRESLHRPALEDLLIGSEANLTCTLTGLRDASGVTFTWTPSSGKSAVQGPPERD 442
                                                                                                                                                                                                                                                      LCGCYSVSSVLSGCAEPWNHGKTFTCTAAYPESKTPLTATLSKSGNTFRPEVHLLPPPSE 374
                                                                                                                                                                                                                                                                         LCGCYSVSSVLPGCAEPWNHGKTFTCTAAYPESKTPLTATLSKSGNTFRPEVHLLPPPSE 502
FQGRVTITADESTSTAYMELSSLRSEDTAVYYCARDPF-----LHYWGQGTLVTV 134
                                                                                                                                                                                                                                                                                                                    ELALNELVTLTCLARGESPKDVLVRWLQGSQELPREKYLTWASRQEPSQGTTTFAVTSIL 434
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    The invention relates to a novel human polynucleotide and the encoded polypeptide. A polynucleotide of the invention may have a use in gene therapy. An oligonucleotide of the invention ADM06202-ADM06773 is useful as a primer for synthesizing the polynucleotide or as a probe for detecting the polynucleotide. The polynucleotides ADM01316-ADM03758 are useful in gene therapy, for developing a diagnostic marker or medicines for regulating their expression and activity, or as a target of gene
                ASGDLYTTSSQLTLPATQCLAGKSVTCHVKHYINPSQDVTVPCPVPSTPPTPSPTP
                                                                                                                                                                                                                                                                                                                                       255 SPSCCHPRLSLHRPALEDLLLGSEANLTCTLTGLRDASGVTFTWTPSSGKSAVQGPPDRD
                                                                                                                                                                                                                                                                                                                                                                                                      for
                                                                                                                                                                                                                                                                                                                                                                                      RVAAEDWKKGDIFSCMVGHEALPLAFIQKIIDRLAGKPTHVNVSVVMAEVDGTCY 489
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      New polynucleotides and polypeptides are useful in gene therapy, developing a diagnostic marker or medicines for regulating their expression and activity, or as a target of gene therapy.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               human; gene therapy; diagnostic marker; pharmaceutical.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Otsuki T, Wakamatsu A,
Hio Y, Otsuka K, Nagai
Otsuka M, Nagahari K, M
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Human protein of the invention SEQ ID NO:4058
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Claim 1; SEQ ID NO 4058; 305pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ADM05373 standard; protein; 496 AA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                12-APR-2002; 2002EP-00008400
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D J, Isono Y, H
Yoshikawa T, O
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            WPI; 2003-723558/69.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  20-MAY-2004
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                                                                                                                                                                                                                                                        315
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85
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                      RESULT 4
ADM05373
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                                                                             434
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          LEOSGAEVKKPGSSVKVSCKASGGSFSSYAINWVRQAQGQGLEWMGGLMPIFGTTNYAQK 202
                374
                                             493
                                                                                                             553
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           84
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Producing polypeptides in chloroplasts, useful in producing antibodíes, by introducing a first recombinant nucleic acid molecule comprising a first polynucleotide encoding at least one polypeptide.
               LCGCYSVSSVLSGCAEPWNHGKTFTCTAAYPESKTPLTATLSKSGNTFRPEVHLLPPPSE
                               434 LCGCYSVSSVLPGCAEPWNHGKTFTCTAAYPESKTPLTATLSKSGNTFRPEVHLLPPPSE
                                                                           ELALNELVTLTCLARGFSPKDVLVRWLQGSQELPREKYLTWASRQEPSQGTTTFAVTSIL
                                                                                               LVQSGAEVKKPGSSVRVSCKASGGTFSSYAISWVRQAPGQGLEWMGGIIPIFGTANYAQK
                                                                                                                                                           RVAAEDWKKGDTFSCMVGHEALPLAFTQKTIDRLAGKPTHVNVSVVMAEVDGTCY 489
                                                                                                                                                                                                                                                                                                                                                      Chloroplast-codon-optimised single chain anti-HSV antibody protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        10;
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                                                                                                                                                                                                                                                                                                                                                                                    plastid; chloroplast; antibody chimera; tetanus toxin; herpes simplex virus; HSV; transgenic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Claim 176; SEQ ID NO 16; 174pp; English.
                                                                                                                                                                                                                                                      ADF68991 standard; protein; 639 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   23-APR-2003; 2003WO-US012997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 23-APR-2002; 2002US-0375129P
19-DEC-2002; 2002US-0434957P
                                                                                                                                                                                                                                                                                                                       (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Mayfield SP, Franklin S;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (SCRI ) SCRIPPS RES INST
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N-PSDB; ADF68990.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 639 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     WO2003091413-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                   Synthetic.
Unidentified.
                                                                                                                                                                                                                                                                                                                       12-FEB-2004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        439;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   06-NOV-2003
                                                                             375
                                                                                                                                           435
                                                                                                                                                                                                                                                                                        ADF68991;
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cell regeneration, membrane protein, signal transduction-related protein,
transcription-related protein, osteoporosis, neurological disease,
                                                                                                                                                                                                                                                                                                                            235
                                                                                                                                                                                                                                                                                                                                        PCPVPSTPPTPSPSTPPTPSPSCCHPRLSLHRPALEDLLLGSEANLTCTLTGLRDASGVT 302
                                                                                                                                                                                                                                                                                                                                                                                                                                                         FTWTPSSGKSAVQGPPERDLCGCYSVSSVLPGCAEPWNHGKTFTCTAAYPESKTPLTATL 362
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           475
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                                                                                                                                                                                                        LEWWGGIIPIFGTANYAQKFQGRVTITADESTSTAYMELSSLRSEDTAVYYCAR---- 119
                                                                                                                                                                                                                         64 LEWMGGIIPIFGSTDYLWKYQGRVIITADESTRTVYMEVTSLTVEDTALYFCARGGRRPY 123
                                                                                                                                                                                                                                                                                                                                                                                                                                         FTWTPSSGKSAVQGPPDRDLCGCYSVSSVLSGCAEPWNHGKTFTCTAAYPESKTPLTATL 355
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             422
                                                                                                                                                  65
                                                                                                                                                                           63
therapy. The proteins ADM03759-ADM06201 encoded by the polynucleotides are useful as pharmaceutical agents. The present sequence represents a protein sequence of the invention.
                                                                                                                                                                 124 RNGFDPF-DVWGQGTRVSVSSASPTSPKVFPLSLCGTQPDGNVVIACLVQGFFPQEPLSV
                                                                                                                                                                                                                                                                                                                                                                                  PCPVPSTPPTPSPSTPPTPSPSCCHPRLSLHRPALEDLLLGSEANLTCTLTGLRDASGVT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  356 SKSGNTFRPEVHLLPPPSEELALNELVTLTCLARGFSPKDVLVRWLQGSQELPREKYLTW
                                                                                                                                                6 FLWALVISTCLEFSMAQVQLVQSGAEVKKPGSSVRVSCKASGGTFSSYAISWVRQAPGQG
                                                                                                                                                                                                                                                                   120 ----DPFLHYWGQGTLVTVSTASPTSPKVFPLSLCSTQPDGNVVIACLVQGFFPQEPLSV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   363 SKSGNTFRPEVHLLPPPSEELALNELVTLTCLARGFSPKDVLVRWLQGSQELPREKYLTW
                                                                                                                                                                                                                                                                                                                         TWSESGQGVTARNFPPSQDASGDLYTTSSQLTLPATQCLAGKSVTCHVKHYTNPSQDVTV
                                                                                                                       Gaps
                                                                                     Query Match

88.2%; Score 2302; DB 7; Length 496;
Best Local Similarity 87.9%; Pred. No. 4e-125;
Matches 434; Conservative 22; Mismatches 24; Indels 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Human protein encoded by clone PEBLM20001800.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ADB64852 standard; protein; 496
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           05-NOV-2001; 2001JP-00379298.
25-JAN-2002; 2002US-00350978.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              28-MAR-2002; 2002EP-00007401
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NVSVVMAEVDGTCY 489
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 496 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  cancer; tumour.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        EP1308459-A2
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The invention discloses a polynucleotide comprising a sequence selected from 1970 fully defined nucleotide sequences which encode novel colypeptides. Also claimed is a polypeptide encoded by the polypeptide or peptide, an antibody binding to the polypeptide or peptide of the polynucleotide, immunologically assaying the polypeptide or peptide or the polynucleotide by contacting the polypeptide or peptide or with the antibody of the encoded protein, and observing the binding between the two, a transformant carrying the polynucleotide in an expressible manner and an antisense polynucleotide. The oligonucleotide in an concept of or spring the polynucleotide in an expressible manner and an antisense polynucleotide. The oligonucleotide of sa probe is useful as paramaceutical agents and many disease-related or proteins are useful as pharmaceutical agents and many disease-related of genes may be included in them, for developing a diagnostic marker or medicines for regulation of their expression and activity, or as targets of gene therapy. The genes are involved in tissue and/or call cregeneration. Membrane proteins, signal transduction-related proteins, creamcription-related proteins, signal transduction-related proteins, concoding them can be used as indicators for diseases (e.g. osteoporosis, neurological diseases, cancer, tumours. The CDNA may be used to regulate the activity or expression of the invention. Note: Some of the sequence presented is a protein of the invention. Note: Some of the specification, but is based on sequence information supplied by the specification, but is based on sequence information supplied by the
                                                          Otsuki T, Wakamatsu A, Sato H, Ishii S;
Hio Y, Otsuka K, Nagai K, Irie R, Tamechika I;
Otsuka M, Nagahari K, Masuho Y;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ERDLCGCYSVSSVLPGCAEPWNHGKTFTCTAAYPESKTPLTATLSKSGNTFRPEVHLLPP 378
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 81 YAQKFQGRVTITADESTSTAYMELSSLRSEDTAVYYCARDPF-----LHYWGQGTL 131
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PSEELALNELVTLTCLARGFSPKDVLVRWLOGSQELPREKYLTWASRQEPSQGTTTFAVT 431
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       VIVSTASPISPKVFPLSLCSTQPDGNVVIACLVQGFFPQEPLSVIWSESGQGVTARNFPP 191
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             251
                                                                                                                                                                                                         New polynucleotides and polypeptides, useful for developing a diagnostic marker or medicines for regulation of their expression and activity, or as targets of gene therapy.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PTPSPSCCHPRLSLHRPALEDLLLGSEANLTCTLTGLRDASGVTFTWTPSSGKSAVQPP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      19 SQEQLVQSGAEVKRPGASVKITCKAPGHTFSSYHYHWVRQAPGQGLEWLGIINPRGGQTT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                139 VIVSAASPISPKVFPLSLCSTQPDGNVVIACLVQGFFPQEPLSVIWSESGQGVTARNFPP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               21 AQVQLVQSGAEVKKPGSSVRVSCKASGGTFSSYAISWVRQAPGQGLEWMGGIIPIFGTAN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PTPSPSCCHPRLSLHRPALEDLLLGSEANLTCTLTGLRDASGVTFTWTPSSGKSAVQGPP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  26; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     87.4%; Score 2281.5; DB 7.
90.0%; Pred. No. 6.1e-124;
iive 13; Mismatches 26;
(HELI-) HELIX RES INST.
(REAS-) RES ASSOC BIOTECHNOLOGY.
                                                                                                                                                                                                                                                                                                      Claim 1; Page; 222pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Matches 430; Conservative
                                                             Sugiyama T,
                                                                                 Yamamoto J, Isono Y,
Seki N, Yoshikawa T,
                                                                                                                                                   2003-450961/43
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N-PSDB; ADB62882
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DLCGCYSVSSVLPGCAEPWINGKTFTCTAAXPESKTPLTATLSKSGNTFRPEVHLLPPPS 379
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                                                                                                         PSPSCCHPRLSLHRPALEDLLLGSEANLTCTLTGLRDASGVTFTWTPSSCKSAVQGPPER
    DASGDLYTTSSQLTLPATQCLAGKSVTCHVKHYTNPSQDVTVPCPVPSTPPTPSPSTPPT
                          DASGDLYTTSSQLTLPATQCLAGKSVTCHVKHYTNPSQDVTVPCPVPSTPPTPSPSTPPT
                                                                                                                                                                      DLCGCYSVSSVLSGCAEPWNHGKTFTCTAAYPESKTPLTATLSKSGNTFRPEVHLLPPPS
                                                                                                                                                                                                                                                     EELALNELVTLTCLARGFSPKDVLVRWLQGSQELPREKYLTWASRQEPSQGTTTFAVTSI
                                                                                                                                                                                                                                                                             EELALNELVTLTCLARGFSPKDVLVRWLQGSQELPREKYLTWASRQEPSQGTTTFAVTS1
                                                                                   PSPSCCHPRLSLHRPALEDLLLGSEANLTCTLTGLRDASGVTFTWTPSSGKSAVQGPPDR
                                                                                                                                                                                                                                                                                                                                                              LRVAAEDWKKGDTFSCMVGHEALPLAFTQKTIDRLAGKPTHVNVSVVMAEVDGTCY 489
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        New polynucleotides and polypeptides are useful in gene therapy, developing a diagnostic marker or medicines for regulating their expression and activity, or as a target of gene therapy.
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Hio Y, Otsuka K, Nagai K, Irie R,
Otsuka M, Nagahari K, Masuho Y;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             human; gene therapy; diagnostic marker; pharmaceutical.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Human protein of the invention SEQ ID NO:4245.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ADM05560 standard; protein; 502
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87.2%;
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Seki N, Yoshikawa T,
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Best Local Similarity
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                                                                                                                          260
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Hio Y, Otsuka K, Nagai K, Irie R, Tamechika I;
Otsuka M, Nagahari K, Masuho Y;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    133
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SQKFRGRVSWIRDISIGIVYMELISIRLDDTAVYYCAGEADSAVRIWAPPDYWGGGGSVT 139
PSEELALNELVTLTCLARGFSPKDVLVRWLQGSQELPREKYLTWASRQEPSQGTTTFAVT 438
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           134 VSTASPISPKVFPLSLCSTQPDGNVVIACLVQGFFPQEPLSVTWSESGQGVTARNFPPSQ 193
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             The invention relates to a novel human polynucleotide and the encoded polypeptide. A polynucleotide of the invention may have a use in gene therapy. An oligonucleotide of the invention ADM06202-ADM06773 is useful as a primer for synthesizing the polynucleotide or as a probe for detecting the polynucleotide. The polynucleotides ADM01316-ADM03758 are useful in gene therapy, for developing a diagnostic marker or medicines for regulating their expression and activity, or as a target of gene therapy. The proteins ADM03759-ADM06201 encoded by the polynucleotides are useful as pharmaccutical agents. The present sequence represents a protein sequence of the invention.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               82 AQKFQGRVTITADESTSTAYMELSSLRSEDTAVYYCARD-----PFLHYWGQGTLVT
                                                               SILRVAAEDWKKGDTFSCMVGHEALPLAFTQKTIDRLAGKPTHVNVSVVMAEVDGTCY
                                       SILRVAAEDWKKGDTFSCMVGHEALPLAFTQKTIDRLAGKPTHVNVSVVMAEVDGTCY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     New polynucleotides and polypeptides are useful in gene therapy, developing a diagnostic marker or medicines for regulating their expression and activity, or as a target of gene therapy.
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                                                                                                                                                                                                                                                                                                                                                          human; gene therapy; diagnostic marker; pharmaceutical.
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89.7%; Pred. No. 1.3e-123;
                                                                                                                                                                                                                                                                                                                Human protein of the invention SEQ ID NO:4085.
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Seki N, Yoshikawa T,
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N-PSDB; ADM02957.
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Best Local Simi
Matches 427;
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                                                                                                                                                                                                                             ADM05400;
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Tamechika I;

Ishii S;

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09-SEP-2004 (first entry)
  N-PSDB; ADR06496
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                                                                    -----FLHYWGQGTLVTVSTASPTSPKVFPLSLCSTQPDGNVVIACLVQGFFPQ 170
                                                                                                           124 IDLSCFTSGVYGLGLWGQGTWVWVSSASPTSFKVFPLSLCSTQPDGWVVIACLVQGFFPQ 183
                                                                                                                                      EPLSVTWSESGQGVTARNFPPSQDASGDLYTTSSQLTLPATQCLAGKSVTCHVKHYTNPS 230
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                                                                                                                                                                              QDVTVPCPVPSTPPTPSPSTPPTPSPSCCHPRLSLHRPALEDLLLGSEANLTCTLTGLRD 290
                                                                                                                                                                                      244 QDVTVPCPVPSTPPTPSPSTPPTPSPSCCHPRISLHRPALEDLLIGSEANLTCTLTGLRD 303
                                                                                                                                                                                                                               304 ASGVIFTWTPSSGKSAVQGPPERDLCGCYSVSSVLPGCAEPWNHGKTFTCTAAYPESKTP 363
                                                                                                                                                                                                                                                                    424 KYLTWASRQEPSQGTTTFAVTSILRVAAEDWKKGDTFSCWVGHBALPLAFTQKTIDRLAG 483
                                                                                                                                                                                                                                                                                                 411 KYLTWASRQEPSQGTTTFAVTSILRVAAEDWKKGDTFSCMVGHEALPLAFTQKTIDRLAG 470
                                       63
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        human; oligo-capping method; diagnostic marker; gene therapy; osteoporosis; neurological disease; Alzheimer's disease; Parkinson's disease; dementia; short memory; cancer; sense or motor function; enotional reaction; fear response; panic; osteopathic; neuroprotective; nootropic; antiparkinsonian; cytostatic;
                              66 LEWMGGIIPIFGTANYAQKFQGRVTITADESTSTAYMELSSLRSEDTAVYYCA-RDP---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Otsuki T;
                  FLWALVISTCLEFSMAQVQLVQSGAEVKKPGSSVRVSCKASGGTFSSYAISWVRQAPGQG
                                                                                                                                                   ASGVTFTWTPSSGKSAVQGPPDRDLCGCYSVSSVLSGCAEPWNHGKTFTCTAAYPESKTP
                                                                                                                                                                                                                                                           LTATLSKSGNTFRPEVHLLPPPSEELALNELVTLTCLARGFSPKDVLVRWLQGSQELPRE
 Gaps
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  18;
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 30;
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Nagai K, Irie R;
 16; Mismatches
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                                                                                                                                                                                                                                                                                                                                         471 KPTHVNVSVVMAEVDGTCY 489
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                                                                                                                                                                                                                                                                                                                                                    484 KPTHVNVSVVMAEVDGTCY
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                                                                                                                                                                                                                                                                                                                                                                                                                                                 (first entry)
435; Conservative
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Wakamatsu A, Ishii S,
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This invention relates to novel, isolated full length human cDNA molecules and the encoded proteins thereof. Specifically, it refers to CDNA clones obtained by an oligo-capping method, where none of these clones are identical to any known human mRNAs. The present invention describes an immunoassay to identify agonists and antagonists, as well as antibodies, antisense molecules and siRNAs that can all be used to bind to and modulate expression of the CDNA molecules. As such, these molecules are useful for diagnostic markers or therapeutic targets for the various diseases or morbid states. In particular, they are useful in gene therapy for treating osteoporosis, neurological disease, Alzheimer's disease, Parkinson's disease, dementia, short memory and various cancers,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 as well as for maintaining equilibrium of sense or motor function, and for treating emotional reaction, fear response and panic. Accordingly, they exhibit osceppathic, neuroprotective, nootropic, antiparkinsonian, cytostatic and tranquiliser activities. This polypeptide is a protein encoded by a full length human cDNA sequence of the invention. NOTE: This sequence is not given in the sequence listing of the specification but can be obtained on CD-ROM from the Buropean Patent Office, Vienna Sub-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          138
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New 1995 cDNA, useful for treating osteoporosis, neurological diseases, Alzheimer's diseases, Parkinson's diseases, dementia and various cancers.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  78
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        21 AQVQLVQSGAEVKKPGSSVRVSCKASGGTFSSYAISWVRQAPGQGLEWMGGIIPIFGTAN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  19 SQAQLVQSGABAKKPGASVKISCKASGYPPSGYVLHWLRQAPGQGLEWLGSITAGYDATK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       VTVSTASPTSPKVFPLSLCSTQPDGNVVIACLVQGFFPQEPLSVTWSESGQGVTARNFPP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SODASGDLYTTSSQLTLPATQCLAGKSVTCHVKHYTNPSQDVTVPCPVPSTPPTPSPSTP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                81 YAQKFQGRVTITADESTSTAYMELSSLRSEDTAVYYCARDPFLHY------WGQGTL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 8;
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89.1%; Pred. No. 2.3e-123;
iive 14; Mismatches 29;
                                                                                             Claim 1; SEQ ID NO 1958; 2686pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     $
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Best Local Similarity
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Otsuki T, Wakamatsu A, Sato H, Ishii S;
Hio Y, Otsuka K, Nagai K, Irie R, Tamechika I;
Otsuka M, Nagahari K, Masuho Y;
The invention relates to a novel human polynucleotide and the encoded polypeptide. A polynucleotide of the invention may have a use in gene therapy. An oligonucleotide of the invention ADM06202-ADM06773 is useful as a primer for synthesizing the polynucleotide or as a probe for detecting the polynucleotide. The polynucleotides ADM01316-ADM03758 are useful in gene therapy, for developing a diagnostic marker or medicines for regulating their expression and activity, or as a target of gene therapy. The proteins ADM03759-ADM06201 encoded by the polynucleotides are useful as pharmaceutical agents. The present sequence represents a
                                                                                              SQDASGDLYTTSSQLTLPATQCLAGKSVTCHVKHYTNPSQDVTVPCPVPSTPPTPSPSTP
                                                                                                                                                                                       PTPSPSCCHPRLSLHRPALEDLILGSBANLTCTLTGLRDASGVTFTWTPSSGKSAVQGPP
                                                                                                                                                                                                                                                                                                                                                                                 361 PSEELALMELVTLTCLARGESPKDVLVRWLQGSQELPREKYLTWASRQEPSQGTTTFAVT
                                                                                                                                                                 PTPSPSCCHPRLSLHRPALEDLLLGSEANLTCTLTGLRDASGVTFTWTPSSGKSAVQGPP
                                                                                                                                                                                                                                                          DRDLCGCYSVSSVLSGCAEPWNHGKTFTCTAAYPESKTPLTATLSKSGNTFRPEVHLLPP
                                                                                                                                                                                                                                                                                     301 ERDLCGCYSVSSVLPGCAEPWNHGKTFTCTAAYPESKTPLTATLSKSGNTFRPEVHLLPP
                                                                  SODASGDLYTTSSQLTLPATQCLAGKSVTCHVKHYTNPSQDVTVPCPVPSTPPSPSTP
                                                                                                                                                                                                                                                                                                                                                        PSEELALNELVTLTCLARGFSPKDVLVRWLQGSQELPREKYLTWASRQEPSQGTTTFAVT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     numan; gene therapy; diagnostic marker; pharmaceutical
                                                                                                                                                                                                                                                                                                                                                                                                                                                       467
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           421 SILRVAAEDWKKGDTFSCMVGHEALPLAFTQKTIDR 456
                                                                                                                                                                                                                                                                                                                                                                                                                                                       SILRVAAEDWKKGDTFSCMVGHEALPLAFTQKTIDR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Human protein of the invention SEQ ID NO:4277.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Claim 1; SEQ ID NO 4277; 305pp; English.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ADM05592 standard; protein; 495
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Isogai T, Sugiyama T,
Yamamoto J, Isono Y,
Seki N, Yoshikawa T,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   WPI; 2003-723558/69.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        The invention relates to the production of immunoglobulins in plants, wherein at least a portion of the glycans attached to the immunoglobulins at lack fucose. The immunoglobulins produced can be of any class (i.e., igG, IgM, IgM, IgE or IgD) and is especially an anti-herpes simplex virus (HSV) antibody or an anti-alphavbeta3, alphavbeta5 dual integrin also relates to constructs, plasmids and vectors for producing the immunoglobulins; transformed plant cells, calli, plant tissues and whole plants for producing the immunoglobulins; the immunoglobulins methods for tradicting the immunoglobulins. The immunoglobulins of the invention may be use of such immunoglobulins of the invention may be use of such immunoglobulins of the invention may be used to treat HSV infection or tumour anglogenesis. The invention may be used to treat HSV infection or tumour anglogenesis. The invention contaminants such as viruses and elimination of pathogenic contaminants such as viruses and elimination of pathogenic contaminants such as viruses and elimination of pathogenic immunoglobulin may not be functional in animals. The present sequence represents the heavy chain (without tailplece) of the human anti-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Novel plant-produced immunoglobulin having glycopeptide or glycan profile with reduced fucosylation, useful for treating herpes simplex virus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                61 AQKFQDRLTITADVSTSTAYMQLSGLTYEDTAMYXCARVAYMLEPTVTAGGLDVWGQGTL 120
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                                                         Transgenic plant; immunoglobulin production; recombinant production; glycosylation; fucose; glycan; virucide; immunotherapy; herpes simplex virus; HSV1; HSV2; human; monoclonal antibody HX8; IgA; heavy chain; antibody.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Briggs K, Glancy T, Hein MB, Hiatt AC, Karnoup AL, Anderson WHK;
Pareddy D, Petolino J, Rubin-Wilson B, Taylor D, Roberts JL;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
                   Human anti-HSV antibody HX8 heavy chain (without tailpiece), SEQ:6.
                                                                                                                                                                                                                                                                              /note= "N-glycosylated. This residue is in the CH2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               10;
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93.0%; Pred. No. 1.3
:ive 11; Mismatches
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                                                                                                                                                                                                                                 Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (DOWC ) DOW CHEM CO.
(DOWC ) DOW AGROSCIENCES LLC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              27-NOV-2002; 2002US-0429385P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                  28-NOV-2003; 2003WO-US037905
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (EPIC-) EPICYTE PHARM INC.
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Best Local Similarity 93.0<sup>3</sup>
Matches 424; Conservative
                                                                                                                                                                                                                                                                                                       region"
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Modified-site
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     433 ILRVAAEDWKKGDTFSCMVGHEALPLAFTQKTIDRLAGKPTHVNVSVVMAEVDGTCY 489
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ILRVAABEDWKKGDIFSCWVGHEALPLAFTQKTIDRLAGKPTHVNVSVVMAEVDGTCY 495
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                                                                                                                   21 AQVQLVQSGAEVKKPGSSVRVSCKASGGTFSSYAISWVRQAPGQGLEWMGGIIPIFGTAN
                                                                                                                                                19 SQAQLVQSGAEVKKRGASLKISCKASGYIFSTFAVHWVRQAPGQRLQWLGWIDAATGNTR
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                    Length 495,
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               85.4%; Score 2230; DB 7; Length 4 87.8%; Pred. No. 5.8e-121; ive 18; Mismatches 32; Indels
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Nagai K, Irie R;
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09-MAY-2003; 2003JP-00131452
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                                      Best Local Similarity 87.84
Matches 419; Conservative
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Wakamatsu A, Ishii S,
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N-PSDB; ADR08293.
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This invention relates to novel, isolated full length human cDNA molecules and the encoded proteins thereof. Specifically, it refers to constant obtained by an oligo-capping method, where none of those clones are identical to any known human mRNAs. The present invention describes an immunoassay to identify agonists and antagonists, as well as cartibodise, antisense molecules and siRNAs that can all be used to bind to and modulate expression of the CDNA molecules. As such, these concerns and modulate expression of the CDNA molecules. As such, these concerns are useful for diagnostic markers or therapeutic targets for molecules are useful for diagnostic markers or therapeutic targets for concerns of motor functionary and sisease, parkinson's disease, and modulate services of moreopolicial disease. Alzheimer's disease, parkinson's disease, dementia, short memory and various cancers, as well as for maintaining equilibrium of sense or motor function, and for treating emotional reaction, fear response and panic. Accordingly, they exhibit osteopathic, neuroprotective, nocropic, antiparkinsonian, cytostatic and tranquiliser activities. This sequence is not given in the sequence of the invention. NOTE: This sequence is not given in the sequence listing of the specification but the sequence of the invention but the sequence is not of the specification but the sequence of the specification but the sequence is not of the specification but the sequence of the specification but the sequence is not of the specification but the sequence of t
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New 1995 cDNA, useful for treating osteoporosis, neurological diseases, Alzheimer's diseases, Parkinson's diseases, dementia and various cancers
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                                                                                                                           Claim 1; SEQ ID NO 3755; 2686pp; English.
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183 SESGGGVTARNFPPSQDASGDLYTTSSQLTLPATQCLAGKSVTCHVKHYTNPSQDVTVPC 242
                                                                                                                                                                      243 PVPSTPPTPSPSTPPTPSPSCCHPRLSLHRPALEDLLLGSEANLTCTLTGLRDASGVTFT 302
                                                                                                                                                                                                                             WTPSSGKSAVOGPPDRDLCGCYSVSSVLSGCAEPWNHGKTFTCTAAYPESKTPLTATLSK 357
                                                                                                                                                                                                                                                 303 WTPSSGKSAVQGPPERDLCGCYSVSSVLPGCAEPWNHGKTFTCTAAYPESKTPLTATLSK 362
                                                                                                                                                                                                                                                                                                      358 SGNTFRPEVHLLPPPSEELALNELVTLTCLARGFSPKDVLVRWLQGSQELPREKYLTWAS 417
                                                                                                                                                                                                                                                                                                                                                                              ROEPSOGTTTFAVTSILRVAAEDWKKGDTFSCMVGHEALPLAFTQKTIDRLAGKPTHVNV 477
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                                                                                                                                                                                                                                                                                                                              SGNTFRPEVHLLPPPSEELALNELVTLTCLARGFSPKDVLVRWLQGSQELPREKYLTWAS
                                                                                                                                                  PVPSTPPTPSPSTPPTPSPSCCHPRLSLHRPALEDLLLGSEANLTCTLTGLRDASGVTFT
                                                                         SESGOGVTARNFPPSQDASGDLYTTSSQLTLPATQCLAGKSVTCHVKHYTNPSQDVTVPC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            human; NOVX; cardiomyopathy; atherosclerosis; cancer; diabetes; inflammation; autoimmune disorder; allergy; blood disorder; acquired immunodeficiency syndrome; AIDS; obesity; asthma; immunoglobulin (Ig)A nephropathy; cirrhosis; arthritis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Human NOVX protein homologue SegID 798.
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02-FEB-2001; 2001US-0266406P.

07-FEB-2001; 2001US-026675P.

07-FEB-2001; 2001US-026675P.

07-FEB-2001; 2001US-0267057P.

08-FEB-2001; 2001US-026795P.

09-FEB-2001; 2001US-0268974P.

15-FEB-2001; 2001US-0268974P.

26-FEB-2001; 2001US-0268974P.
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2001US-0275950P.
2001US-0275989P.
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26-FEB-2001; 2
27-FEB-2001; 2
27-FEB-2001; 2
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02-MAR-2001;
14-MAR-2001;
14-MAR-2001;
14-MAR-2001;
14-MAR-2001;
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length cDNAs defined in the specification. Where a primer set comprises:

(a) an oligo-dr primer and an oligonucleotide comprises one of the 5602
complementary strand of a polynucleotide which comprises one of the 5602
nucleotide sequences defined in the specification, where the
complementary strand of a polynucleotide which comprises a 5'-end
complementary strand of a polynucleotide which comprises a 5'-end
complementary strand of a polynucleotide which comprises a 5'-end
complementary strand of a polynucleotide which comprises a 5'-end
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coligonucleotide comprises a 1'-end sequence of polynucleotide of the 5'-end sequence of the 6'-end sequence of the 5'-end sequence of the 5'-end sequence of the 6'-end sequence of 5'-end 5'-end sequence of 5'-end 5
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GLEWMGGIIPIFGTANYAQKFQGRVTITADESTSTAYMELSSLRSEDTAVYYCARDFF-- 122
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               8; Gaps
                                                                                                              Human; primer; detection; diagnosis; antisense therapy; gene therapy
                                                                                                                                                                                                                                                                                                                                                                                                                                                             Yamamoto J;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match 84.8%; Score 2215; DB 4; Length 494; Best Local Similarity 84.8%; Pred. No. 4.2e-120; Matches 417; Conservative 26; Mismatches 41; Indels E
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Claim 8; SEQ ID NO 18518; 2537pp + Sequence Listing; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                             Saito K, Ya
Otsuki T;
                                                                                                                                                                                                                                                                                                                                                                                                                                                           Isogai T, Nishikawa T, Hayashi K, S
, Sugiyama T, Wakamatsu A, Nagai K,
                                                                           Human protein sequence SEQ ID NO:18518.
                                                                                                                                                                                                                                                                                                      29-JUL-1999; 99JP-00248036.
27-A021999; 99JP-00300253.
11-JAN-2000; 2000JP-00118776.
02-MAY-2000; 2000JP-00183767.
                                                                                                                                                                                                                                                                   28-JUL-2000; 2000EP-00116126
                                                                                                                                                                                                                                                                                                                                                                                  09-JUN-2000; 2000JP-00241899
                                     (first entry)
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Tchernev VT, Spytek KA, Zerhusen BD, Patturajan M,
Li L, Gangolli EA, Padigaru M, Anderson DW, Rastell
Gerlach VL, Taupier RJ, Gusev VY, Colman SD, Wolenc
Furtak K, Grosse WM, Alsobrook JP, Lepley DM, Riege
                                 2001US-0278775F
2001US-0278778P
2001US-0279882F
2001US-0280447P
2001US-0280447P
2001US-028292F
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2001US-0294473P.
2001US-0296964P.
2001US-0299334P.
2001US-029334P.
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2001US-0312908P.
2001US-0313390P.
2001US-0315470P.
      2001US-0276450P.
2001US-0276397P.
2001US-0276768P.
2001US-0278652P.
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2001US-0323379P.
2001US-0330245P.
2001US-0330308P.
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2001US-0288327P.
                                                                                    2001US-0285133P
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                            20-MAR-2001;
                                  26-MAR-2001;
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                                                                     11-APR-2001;
11-APR-2001;
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                                                                                                                                     18-JUN-2001;
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neurogenesis, wound healing and angiogenesis. The nucleic acids are also used as in chromosome mapping, tissue typing, preventive medicine and pharmacogenomics. This polypeptide is a homologue of a human NOVX protein
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                                                                                                                                                                                                                                             64
                                                                                                                                                                                                                                                                                                                                                                                                                                                   123 AICYGFSPWGQGTLVTVSSASPTSPKVFPLSLCSTQPDGNVVIACLVQGFFPQEPLSVTW
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          303 WTPSSGKSAVQGPPERDLCGCYSVSSVLPGCAEPWNHGKTFTCTAAYPESKTPLTATLSK
                                                                                                                                                                                                                                          5 GFLWALVISTCLEFSWAQVQLVQSGAEVKKPGSSVRVSCKASGGTFSSYAISWVRQAPGQ
                                                                                                                                                                                                                                                                                                                                 65 GLEWMGGIIPIFGTANYAQKFQGRVTITADESTSTAYMELSSLRSEDTAVYYCARDPF--
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   183 SESGGGVTARNFPPSQDASGDLYTTSSQLTLPATQCLAGKSVTCHVK4YTNPSQDVTVPC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       243 PVPSTPPTPSPSTPPTPSPSCCHPRLSLHRPALEDLLLGSEANLTCTLTGLRDASGVTFT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   298 WTPSSGKSAVQGPPDRDLCGCYSVSSVLSGCAEPWNHGKTFTCTAAYPESKTPLTATLSK
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       363 SGNTFRPEVHLLPPPSEELALNELVILTCLARGFSPKDVLVRWLQGSQELPREKYLTWAS
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                                                                                                                                                                                                                                                                                      4 GLRWVFLVA-FLEGVQCEVQLVESGGGLVKPGGSLRLSCAASGLSFSTYAMNWVRQAPGK
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                                                                                                                                                                                                 Gaps
                                                                                                                                                                                                 8
                                                                                                                                                      Length 494;
                                                                                                                                                      Query Match
84.8%; Score 2215; DB 5; Length 4
Best Local Similarity 84.8%; Pred. No. 4.2e-120;
Matches 417; Conservative 26; Mismatches 41; Indels
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                                                                    of the invention.
                                                                                                             Sequence 494 AA;
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New NOVX polypeptides and nucleic acids, useful for preventing or treating NOVX-associated disorders, e.g. cancer, cardiomyopathy, atherosclerosis, or diabetes, and in chromosome mapping, tissue typing or

Burgess CE;

Anderson DW, Rastelli L, Miller CE, t, Colman SD, Wolenc AR, Pena CEA, TP, Lepley DM, Rieger DK, Burgess CE

Shimkets RA;

Disclosure; SEQ ID NO 798; 1498pp; English.

This invention relates to a novel nucleic acids, and encoded polypeptides thereof, which have properties related to the stimulation of biochemical cor physiological responses in a cell, tissue, organ or organism.

Cor physiological responses in a cell, tissue, organ or organism.

Capecifically, it refers to the use of biologically active fragments for diagnostic and prognostic assays and furthermore in the treatment of diverse pathological conditions. The present invention describes novel thuman and murine NOVX proteins, as well as methods to modulate their expression using antisense oligos, ribozymes and peptide nucleic acids. The NOVX polypeptides, polynucleotides and antibodies are useful in treating or preventing NOVX-associated disorders, e.g. cardiomyopathy, atherosclerosis, cancer and diabetees. Furthermore, they may be used in treating or preventing diseases such as inflammation, autoimmune of disorders, allergies, blood disorders, acquired immunodeficiency syndrome of disorders, allergies, blood disorders, acquired immunodeficiency syndrome of disorders, allergies, manipully, these molecules have many activities including cycostatic, cardiant, antidiabetic, antiarteriosclerotic, anorectic, and epilepsy, complexepsy, antiarthritic, hapetotropy, antiarthritic, hapetotropy, antiarthritic, hapetotropy, antiparteriosclerotic, antiarthritic, neuroprotective, notropic, antiarthritic, hey are useful in screening creamant and anticonvulsant. In addition, they are useful in screening creample, assays to identify small molecules that modulate or inhibit, for example,

osteopathic, neuroprotective, nootropic, antiparkinsonian; cytostatic, gene therapy, diagnostic marker; morbid state; osteoporosis; neurological disease; Alzheimer's disease; Parkinson's disease; dementia; 21-JAN-2004; 2004EP-00001196. 21-JAN-2003; 2003JP-00102206. 09-MAY-2003; 2003JP-00131392. Homo sapiens. EP1440981-A2 cancer

Novel human protein sequence #861.

07-OCT-2004 (first entry)

ADQ65888;

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Human; full length cDNA; cDNA synthesis; oligo-capping
                                                                                                                                                     (HELI-) HELIX RES INST
                                                                                                                                                                                                         WPI; 2001-524255/58
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les 417; Conserv
                                                                                                                                                                                                                     N-PSDB; AAK94202
                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 493 AA;
                                           EP1130094-A2
                                                                15-SEP-2001
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                                                                                                                                                The invention relates to 2495 novel polynucleotides (I) and their encoded polypeptides, sequences hybridizing to these nucleotides, sequences encoding partial polypeptides and sequences having 70% to 90% identity to the nucleotide and protein sequences. The nucleotides and polypeptides are useful as diagnostic markers or therapeutic target for the diseases or mothlo floates. They are also useful for treating osteoporosis, neurological diseases, Alzheimer's diseases, Parkinson's diseases, dementia and various cancers. This sequence corresponds to a protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 318
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                                                                                                                                                                                                                                                                                                                                                                                                                       VTVSTASPTSPKVFPLSLCSTQPDGNVVIACLVQGFFPQEPLSVTWSESGQGVTARNFPP 191
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SQDASGDLYTTSSQLTLPATQCLAGKSVTCHVKHYTNPSQDVTVPCPVPSTPPTPSPSTF 251
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PTPSPSCCHPRLSLHRPALEDLLIGSEANLTCTLTGLRDASGVTFTWTPSSGKSAVQGPP 311
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DRDLCGCYSVSSVLSGCAEPWNHGKTFTCTAAYPESKTPLTATLSKSGNTFRPEVHLLPP 371
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PSEELALNELVTLTCLARGFSPKDVLVRWLQGSQELPREKYLTWASRQEPSQGTTTFAVT 431
                                                                                              Novel 2495 cDNA, useful for treating osteoporosis, neurological diseases, Alzheimer's diseases, Parkinson's diseases, dementia and various cancers.
                                                                                                                                                                                                                                                                                                                                            SQEQLLQSATEVKQPGDSVKVSCRASEDIFISSYFHWVRQAPGQGLEWMGIINPGGGRTN 78
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PTPSPSCCHPRLSLHRPALEDLLLGSEANLTCTLTGLRDASGVTFTWTPSSGKSAVQGPP
                                                                                                                                                                                                                                                                                                                                 21 AQVQLVQSGAEVKKPGSSVRVSCKASGGTFSSYAISWVRQAPGQGLEWMGGIIPIFGTAN
                                                                                                                                                                                                                                                                                                            9; Gaps
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                                ŝ
                                 Ishii
                                                                                                                                                                                                                                                                                      8; Length 496;
                                                                                                                                                                                                                                                                                                            34; Indels
                                Sato H,
                                                                                                                                                                                                                                                                                   ; Score 2213.5; DB 8; Pred. No. 5.2e-120; 14; Mismatches 34;
                                Wakamatsu A,
                                         Irie R;
                                                                                                                               Claim 1; SEQ ID NO 3049; 2449pp; English
                                Otsuki T,
                                          Nagai K,
          ASSOC BIOTECHNOLOGY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AAM93283 standard, protein; 493
                                                                                                                                                                                                                                                                                      84.8%;
                                                                                                                                                                                                                                                                                   Query Match 84.8%
Best Local Similarity 88.1%
Matches 421; Conservative
                                                                                                                                                                                                                                           sequence of the invention.
                                Sugiyama T,
Isono Y,
                                                               2004-535376/52
                                                                         N-PSDB; ADQ63700
                                                                                                                                                                                                                                                                Sequence 496 AA;
                                          Yamamoto J,
                              Isogai T,
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The invention relates to primers for synthesising full length cDNA clones. 830 cDNA molecules encoding a human protein have been isolated and nucleotide sequences of 5'- and 3'-ends of the cDNA molecules have been determined. Primers for synthesising the full length cDNA are useful for clarifying the function of the protein encoded by the cDNA. The full length clones were obtained by construction of full length enriched cDNA libraries that were synthesised by the oligo-capping method. The primers enable the production of the full length cDNA easily without any special methods. The present sequence is a polypeptide provided in the special specification. Note: The sequence data for this patent did not form part from EPO
                                                                                                                                                                                                                                                                                                                                                                                                                                                         830 Primers useful for synthesizing full length cDNA clones and their use in genetic manipulation.
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                                                                                                                                                                                                                         Ota T, Nishikawa T, Isogai T, Hayashi K, Ishii S, Kawai Y;
Wakamatsu A, Sugiyama T, Nagai K, Kojima S, Otsuki T, Koga
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Disclosure; SEQ ID NO 2764; 1380pp + Sequence Listing; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          84.3%; Score 2201.5; DB 4; Length 493;
84.8%; Pred. No. 2.6e-119;
Live 23; Mismatches 43; Indels 9;
08-JUL-1999; 99JP-00194486.
11-JAN-2000; 2000JP-00118774.
02-MAY-2000; 2000JP-00183765.
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Human polypeptide, SEQ ID NO: 2764

06-NOV-2001

6 6 6

Search completed: October 25, 2005, 11:05:47 Job time: 85.1449 secs

Sequence 4275, Ap Sequence 4081, App Sequence 4081, Ap Sequence 4114, Ap Sequence 4058, Ap Sequence 4245, Ap Sequence 323, App Sequence 55, App Sequence 55, App Sequence 112, App Sequence 122, App Sequence 112, App Sequence 113, App Sequence 114, App Sequence 115, App Sequence 114, App Sequence 115, App Sequence 114, App Sequence 114, App Sequence 114, App Sequence 114, App Sequence 21, App Sequence 215, App Sequence 215,

Title: Perfect score:

Sequence:

OM protein

Run on:

Scoring table:

Searched:

Database

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US-10-644-256-3
| Sequence 3, Application US/10644256
| Sequence 3, Application US/10642241
| Sequence 3, Application US/1064226|
| Publication No. US2005010672241
| GENERAL INFORMATION:
| APPLICANT: Jones, David HA
| APPLICANT: Bout, Abraham
| TITLE OF INVENTION: Efficient Production of IgA in Recombinant Mammalian Cells
| FILE REPRENCE: 2578-6077
| CURRENT APPLICATION NUMBER: US/10/644,256
| PRIOR APPLICATION NUMBER: US 60/129,463
| PRIOR PILING DATE: 2000-04-16
| PRIOR PILING DATE: 1999-04-15
| NUMBER OF SEQ ID NOS: 8
| SOFTWARE: Patentin Version 3.2
| SEQ ID NO 3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      OTHER INFORMATION: Amino acid sequence anti-EpCAM 1gA heavy chain
5 US-10-108-260A-4275
5 US-10-072-012-798
1 US-10-108-260A-4104
5 US-10-108-260A-4104
5 US-10-108-260A-4104
5 US-10-108-260A-424
5 US-10-108-260A-424
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1 US-09-800-729-145
1 US-10-072-145
1 US-10-072-145
1 US-10-072-145
1 US-09-807-729-1
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US-10-072-012-322
US-10-207-655-286
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    FEATURE:
NAME/KEY: MISC_FEATURE
LOCATION: (1) 7(21)
OTHER INFORMATION: leader peptide
       NAME/KEY: MISC_FEATURE
LOCATION: (22)...(136)
OTHER INFORMATION: VH REGION
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NAME/KEY: MISC FEATURE
LOCATION: (137)..(238)
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ORGANISM: artificial

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       Sequence 3, Appli
Sequence 4078, Ap
Sequence 302, App
Sequence 3773, Ap
Sequence 16, Appl
Sequence 16, Appl
Sequence 797, Appl
Sequence 37, Appl
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Sequence 4262, Ap
Sequence 4290, Ap
                                                                                                                               October 25, 2005, 11:07:58 ; Search time 94.7482 Seconds (without alignments) 1555.504 Million cell updates/sec
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                     GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.
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US-10-108-260A-4078
US-09-813-250A-302
US-10-104-047-3773
US-10-108-260A-3028
US-10-047-242-16
US-10-047-242-16
US-10-072-012-97
US-10-1014-047-3243
US-10-108-260A-4262
US-10-108-260A-4262
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1898
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Maximum Match 100%
Listing first 45 summaries
                                                                                               - protein search, using sw model
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Gapop 10.0 , Gapext 0.5
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Maximum DB seq length: 200000000
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US-10-108-260A-4078

Sequence 4078, Application US/10108260A

Publication No. US20040005560A1

GENERAL INFORMATION:
APPLICANT: HELIX RESEARCH INSTITUTE

TITLE OF INVENTION: No. US20040005560A1e1 full length cDNA
FILE REFERENCE: H1-A0106

CURRENT APPLICATION NUMBER: US/10/108,260A

CURRENT FILING DATE: 2002-03-27

NUMBER OF SEQ ID NOS: 5458

SOFTWARE: PatentIn Ver. 2.1

SEQ ID NO 4078

LENGTH: 494
            FEATURE:
NAME/KEY: MISC FEATURE
COCATION: (239)
THEATURE:
NAME/KEY: MISC FEATURE
NAME/KEY: MISC FEATURE
LOCATION: (360)...(489)
COTHER INFORMATION: CH3 Region
US-10-644-256-3
OTHER INFORMATION: CH1
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US-10-108-260A-4078
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                                                                      ALNELVTLTCLARGFSPKDVLVRWLQGSQELPREKYLTWASRQEPSQGTTTFAVTSILRV 300
                                                                                                382 ALNELVTLTCLARGFSPKDVLVRWLQGSQELPREKYLTWASRQEPSQGTTTFAVTSILRV 441
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322 GCYSVSSVLPGCAEPWNHGKTFTCTAAYPESKTPLTATLSKSGNTFRPEVHLLPPPSEEL
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203 GDLYTTSSQLTLPATQCLAGKSVTCHVKHYTNPSQDVTVPCPVPSTPPTFSPSTPPTPSP
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                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT: Human Genome Sciences, Inc.
TITLE OF INVENTION: Albumin Fusion Proteins
FILE REPERENCE: PF546PCT
CURRENT APPLICATION NUMBER: US/09/833,245
CURRENT FILING DATE: 2001-04-12
PRIOR APPLICATION NUMBER: 60/229, 358
PRIOR APPLICATION NUMBER: 60/256, 931
PRIOR FILING DATE: 2000-12-21
PRIOR FILING DATE: 2000-12-21
PRIOR FILING DATE: 2000-04-25
NUMBER OF SEQ ID NOS: 2267
SOFTWARE: PATENTIN Ver. 2.1
SEQ ID NOS: 2267
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                                                                                                                                                                                                                                                                                                                                              ; Sequence 302, Application US/09833245; Publication No. US20040010134A1; GENERAL INFORMATION:
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; ORGANISM: Homo sapiens
US-09-833-245-302
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Best Local Similarity
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US-09-833-245-302
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181 GCXSVSSVLPGCAEPWNHGKTFTCTAAYPESKTPLTATLSKSGNTFRPEVHLLPPPSEEL 240
                                                                                                                                                                  241 ALNELVTLTCLARGFSPKDVLVRWLQGSQELPREKYLTWASRQEPSQGTTTFAVTSILRV 300
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        121 SCCHPRISLHRPALEDLILGSBANLTCTLTGLRDASGVTFTWTPSSGKSAVQGPPDRDLC 180
                                 276 SCCHPRLSLHRPALEDLILGSEANLTCTLTGLRDASGVTFTWTPSSGKSAVQGPPDRDLC 335
                                                                                      GCYSVSSVLSGCAEPWNHGKTFTCTAAYPESKTPLTATLSKSGNTFRPEVHLLPPPSEEL 240
                                                                                                           336 GCYSVSSVLPGCAEPWNHGKTFTCTAAYPESKTPLTATLSKSGNTFRPEVHLLPPPSEEL 395
                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT: LARRICK, JAMES W.
APPLICANT: LARRICK, JAMES W.
APPLICANT: LARRICK, JAMES W.
TITLE OF INVENTION: NOVEL IMMUNOADHESINS FOR TREATING AND PREVENTING VIRAL.
TITLE OF INVENTION: AND BACTERIAL DISEASES
FILE REFERENCE: 030905.0004.CIP1
CURRENT APPLICATION NUMBER: US/10/047,542
CURRENT FILING DATE: 2001-10-26
PRIOR APPLICATION NUMBER: PCT/US01/13932
PRIOR FILING DATE: 2001-04-28
PRIOR FILING DATE: 2000-04-28
NUMBER OF SEQ ID NOS: 101
SOFTWARE: Patentin Ver. 2.1
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'Sequence 16, Application US/10047542
'Publication No. US20020168367A1
'GENERAL INFORMATION:
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TYPE: PRT
ORGANISM: Homo sapiens
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US-10-072-012-797
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                                                                                                                                                                                                                                                                                       Query Match
99.7%; Score 1893; DB 15; Length 497;
Best Local Similarity 99.7%; Pred. No. 7.8e-117;
Matches 352; Conservative 0; Mismatches 1; Indels 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 1893; DB 15; Length 508;
Pred. No. 8e-117;
0; Mismatches 1; Indels 0
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Publication No. US20040005560A1
GENERAL INFORMATION:
APPLICANT: HELIX RESEARCH INSTITUTE
TITLE OF INVERTION: No. US20040005560A1e1 full length cDNA
FILE REFERENCE: H1-A0106
CURRENT APPLICATION NUMBER: US/10/108,260A
CURRENT PILING DATE: 2002-03-27
NUMBER OF SEQ ID NOS: 5458
SOFTWARE: PatentIn Ver. 2.1
TITLE OF INVENTION: No. US20030236392A1e1 full length cDNA FILE REFERENCE: H1-A0105
CURRENT APPLICATION NUMBER: US/10/104,047
CURRENT FILING DATE: 2002-03-25
PRIOR APPLICATION UNMBER:
PRIOR FILING DATE: 2002-03-25
NUMBER OF SEQ ID NOS: 4096
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 3773
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Best Local Similarity 99.7%;
Matches 352; Conservative
                                                                                                                                                                                                        ; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-104-047-3773
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US-10-108-260A-3028
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US-10-108-260A-3028
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         212 GCYSVSSVLPGCAEPWNHGKTFTCTAAXPESKTPLTATLSKSGNTFRPEVHLLPPPSEEL
                                                                                               241 ALNELVTLTCLARGFSPKDVLVRWLQGSQELPREKYLTWASRQEPSQGTTTFAVTSILRV
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; OTHER INFORMATION: Incyte ID No. US20030119737A1 2531065CD1
US-10-221-945-3
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Sequence 3. Application US/10221945
Publication No. US20030119737A1
GENERAL INFORMATION:
APPLICANT: INCYTE GENOMICS, INC.
APPLICANT: HELLY
APPLICANT: HELLY
APPLICANT: HILLMAN, Jennifer L.
APPLICANT: BAUGHN, Mariah R.
TITLE OF INVENTION: HUMAN IMMUNE RESPONSE PROTEINS
FILE REFERENCE: PF-0765 PCT
CURRENT APPLICATION NUMBER: US/10/21,945
CURRENT FILING DATE: 2002-09-16
PRIOR APPLICATION NUMBER: US 60/189,417
PRIOR FILING DATE: 2000-03-15
PRIOR FILING DATE: 2000-03-15
NUMBER OF SEQ 1D NOS: 8
SOFTWARE: PERL PROGRAM
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ORGANISM: Homo sapiens
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LENGTH: 393
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US-10-221-945-3
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                                                                                                                                                                                                 APPLICANT: Gerlach, Charles E.
APPLICANT: Gerlach, Valerie
APPLICANT: Guese, Valddimir Y.
APPLICANT: Globe, Date M. R.
APPLICANT: Bene, Ceal B. A APPLICANT: Globe, Maillam M.
APPLICANT: Alebbrook II, John P.
APPLICANTON NUMBER: 60/265, 102
PRIOR APPLICANTON NUMBER: 60/265, 105
PRIOR APPLICANTON NUMBER: 60/266, 767
PRIOR PRIING DATE: 2001-02-06
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                                                                                         Patturajan, Meera
Shimkets, Richard
APPLICANT: Tchernev, Velizar
APPLICANT: Spytek, Kimberly
APPLICANT: Zerhusen, Bryan
                                                                                                                                                                               Gangolli, Esha
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CORGANISM: Homo sapiens
US-10-072-012-797
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APPLICANT:
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319 GCYSVSSVLPGCAEPWNHGKTFTCTAAYPESKTPLTATLSKSGNTFRPEVHLLPPPSEEL 378
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                              199 GDLYTTSSQLTLPATQCLAGKSVTCHVKHYTNPSQDVTVPCPVPSTPPTPSPSTPPTPSP 258
                                                                                          SCCHPRLSLHRPALEDLLLGSEANLTCTLTGLRDASGVTFTWTPSSGKSAVQGPPDRDLC 180
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length 491;
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Sequence 4290, Application US/10108260A
Publication No. US20040005560A1
GENERAL INFORMATION:
APPLICANT: HELIX RESEARCH INSTITUTE
TITLE OF INVENTION: No. US20040005560A1e1 full length cDNA
FILE REFERENCE: H1-A0106
CURRENT APPLICATION NUMBER: US/10/108,260A
CURRENT FILING DATE: 2002-03-27
NUMBER OF SEQ ID NOS: 5458
SOFTWARE: PATENTIN Ver. 2.1
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, Publication No. US20040005560A1
, GENERAL INFORMATION:
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US-10-108-260A-4275
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ORGANISM: Homo
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; LENGTH: 491
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                                                                                                                                                                                                                                                                                                                                                                                                              Length 491;
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; Publication No. US20040005560A1
; GENERAL INFORMATION:
; TITLE OF INVENTION: No. US20040005560A1e1 full length cDNA
; FILE REFERENCE: H1-A0106
; CURRENT APPLICATION NUMBER: US/10/108,260A
; CURRENT FILING DATE: 2002-03-27
; NUMBER OF SEQ ID NOS: 5458
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 4262
; LENGTH: 491
                                                           APPLICATION TO CONTRACT TO THE SELECT TO THE SELECT TITLE OF INVENTION: No. US20030236392A1e1 full length cDNA FILE REFERENCE: H1-A0105
CURRENT APPLICATION NUMBER: US/10/104,047
CURRENT FILING DATE: 2002-03-25
PRIOR APPLICATION NUMBER:
PRIOR PILING DATE:
NUMBER OF SEQ ID NOS: 4096
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 3343
LENGTH: 491
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Sequence 3243, Application US/10104047
Publication No. US20030236392A1
GENERAL INFORMATION:
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Best Local Similarity 99.4
Matches 351; Conservative
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ORGANISM: Homo sapiens
US-10-104-047-3243
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US-10-108-260A-4262
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APPLICANT: Lepley, Denise M.
APPLICANT: Rieger, Daniel K.
APPLICANT: Burges: Catherine E.
TITLE OF INVENTION: Proteins and Nucleic Acids Encoding Same PILE REPERENCE: 21402-258
CURRENT APPLICATION NUMBER: US/10/072,012
APPLICANT: HELIX RESEARCH INSTITUTE
TITLE OF INVENTION: No. US20040005560Alel full length cDNA
FILE REFERENCE: H1-A0106
CURRENT APPLICATION NUMBER: US/10/108,260A
CURRENT ADDATE: 2002-03-27
NUMBER OF SEQ ID NOS: 5458
SSOFTWARE: Patentin Ver. 2.1
LENGTH: 494
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Publication No. US20040033493A1
GENERAL INFORMATION:
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Gangolli, Esha
Padigaru, Muralidhara
Anderson, David W.
Rastelli, Luca
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APPLICANT: Spytek, Kimberly
APPLICANT: Serhusen, Bryan
APPLICANT: Parturajan, Meera
APPLICANT: Shimkets, Richard
                                                                                                                                                                                        TYPE: PRT

ORGANISM: Homo sapiens

US-10-108-260A-4275
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US-10-072-012-798
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PRIOR APPLICATION NUMBER: 60/265,102
PRIOR PLING DATE: 2002-01-31
PRIOR FILING DATE: 2001-01-30
PRIOR FILING DATE: 2001-01-31
PRIOR PLICATION NUMBER: 60/265,514
PRIOR PLICATION NUMBER: 60/265,517
PRIOR PLING DATE: 2001-01-31
PRIOR PLING DATE: 2001-02-32
PRIOR PLING DATE: 2001-02-02
PRIOR PLING DATE: 2001-02-02
PRIOR PLING DATE: 2001-02-02
PRIOR PLING DATE: 2001-02-05
PRIOR PLING DATE: 2001-02-07
PRIOR PLING DATE: 2001-02-08
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Publication No. US20040005560A1
GENERAL INFORMATION:
APPLICANT: HELIX RESEARCH INSTITUTE
ITLE OF INVENTION: No. US20040005560A1e1 full length cDNA
FILE REPRESENCE: H1-A0106
CURRENT APPLICATION NUMBER: US/10/108,260A
CURRENT FILING DATE: 2002-03-27
NUMBER OF SEQ ID NOS: 5458
SOUTH NOSE PATENTIN Ver. 2.1
SEQ ID NO 4085
LENGTH: 495
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Matches 351; Conservative
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                                                               Length 495;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ; Sequence 4114, Application US/10108260A; Bedication No. US20040005560A1; GENERAL INFORMATION: APPLICANT: HELLIX RESEARCH INSTITUTE TITLE OF INVENTION: No. US20040005560A1e1 full length cDNA; FILE REFERENCE: H1-A0106; CURRENT APPLICATION NUMBER: US/10/108,260A; CURRENT FILING DATE: 2002-03-27; NUMBER OF SEQ ID NOS: 5458; SOFTWARE: Patentin Ver. 2.1; LENGTH: 495; TIVE: PRT
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US-10-108-260A-4114
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US-10-108-260A-4114
TYPE: PRT
ORGANISM: Homo
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This invention relates to novel, isolated full length human cDNA molecules and the encoded proteins thereof. Specifically, it refers to CDNA clones obtained by an oligo-capping method, where none of these clones are identical to any known human mRNAs. The present invention describes an immunoassay to identify agonists and antagonists, as well as antibodies, antisense molecules and siRNAs that can all be used to bind to and modulate expression of the CDNA molecules. As such, these
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GenCore version 5.1.6
(c) 1993 - 2005 Compugen Ltd.
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09-MAY-2003; 2003JP-00131452
                                                                                                                                                                                                                                (first entry)
Isogai T, Yamamoto J,
Wakamatsu A, Ishii S,
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N-PSDB; ADR08293.
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molecules are useful for diagnostic markers or therapeutic targets for the various diseases or morbid states. In particular, they are useful in gene therapy for treating osteoporosis, neurological disease, Alzheimer's disease, Parkinson's disease, dementa, short memory and various cancers, as well as for maintaining equilibrium of sense or motor function, and for treating emotional reaction, fear response and panic. Accordingly, they exhibit osteopathic, neuroprotective, nootropic, antiparkinsonian, cytostatic and tranquiliser activities. This polypeptide is a protein encoded by a full length human cDNA sequence of the invention. NOTE: This sequence is not given in the sequence listing of the specification but can be obtained on CD-ROM from the European Patent Office, Vienna Sub-
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Sequence 492 AA;

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99.7%; Score 1893; DB 8; Length 492;
99.7%; Pred. No. 2.9e-119;
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Ishii S;
R, Tamechika I;
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io Y, Otsuka K, Nagai K, Irie R,
Otsuka M, Nagahari K, Masuho Y;
                                                                                                     human; gene therapy; diagnostic marker; pharmaceutical.
                                                                                Human protein of the invention SEQ ID NO:4078,
                                                                                                                                                                                                                                                          Hio Y, Ot
                   ADM05393 standard; protein; 494
                                                                                                                                                                                                                             (REAS-) RES ASSOC BIOTECHNOLOGY.
                                                                                                                                                                                    12-APR-2002; 2002EP-00008400,
                                                                                                                                                                                                         22-MAR-2002; 2002JP-00137785.
                                                            (first entry)
                                                                                                                                                                                                                                              Isogai T, Sugiyama T,
Yamamoto J, Isono Y,
Seki N, Yoshikawa T,
                                                                                                                                                                                                                                                                                       WPI; 2003-723558/69.
                                                                                                                         Homo sapiens
                                                                                                                                            EP1347046-A1
                                                           20-MAY-2004
                                        ADM05393;
RESULT 2
ADM05393
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120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               osteopathic; neuroprotective; nootropic; antiparkinsonian; cytostatic; gene therapy; diagnostic marker; morbid state; osteoporosis; neurological disease; Alzheimer's disease; Parkinson's disease; dementia;
                                                                                                                 The invention relates to a novel human polynucleotide and the encoded polypeptide. A polynucleotide of the invention may have a use in gene therapy. An oligonucleotide of the invention ADM06202-ADM06773 is useful as a primer for synthesizing the polynucleotide or as a probe for detecting the polynucleotide. The polynucleotide or as a probe for useful in gene therapy, for developing a diagnostic marker or medicines for regularing their expression and activity, or as a target of gene therapy. The proteins ADM03759-ADM06201 encoded by the polynucleotides are useful as pharmaceutical agents. The present sequence represents a protein sequence of the invention.
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                           New polynucleotides and polypeptides are useful in gene therapy, developing a diagnostic marker or medicines for regulating their expression and activity, or as a target of gene therapy.
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                                                                                                                                                                                                                                                                                                                        Score 1893; DB 7;
Pred. No. 2.9e-119;
0; Mismatches 1;
                                                                                      Claim 1; SEQ ID NO 4078; 305pp; English
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Best Local Similarity 99,77
Matches 352, Conservative
N-PSDB; ADM02950.
                                                                                                                                                                                                                                                                                           Sequence 494 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SCCHPRLSLHRPALEDLLLGSEANLTCTLTGLRDASGVTFTWTPSSGKSAVQGPPDRDLC 180
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                                                                                                                                                 Novel 2495 cDNA, useful for treating osteoporosis, neurological diseases, Alzheimer's diseases, Parkinson's diseases, dementia and various cancers.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                            ASPTSPKVFPLSLCSTQPDGNVVIACLVQGFFPQEPLSVTWSESGQGVTARNFPPSQDAS
                                                                                                                                                                                                                                                                                                                                                                                                                                           1 ASPTSPKVFPLSLCSTQPDGNVVIACLVQGFFPQEPLSVTWSESGQGVTARNFPPSQDAS
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                                                                   Wakamatsu A, Sato H, Ishii S;
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                                                                                                                                                                                                                                                                                                                                                                                    99.7%; Score 1893; DB 8; Length 494; 99.7%; Pred. No. 2.9e-119; ive 0; Mismatches 1; Indels (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Human gene 4-encoded secreted protein HTOIQ42, SEQ ID NO:95.
                                                                                                                                                                                        Claim 1; SEQ ID NO 2851; 2449pp; English
                                                                   Otsuki T, Wakam
Nagai K, Irie R;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AAG62159 standard; protein; 495 AA
                                      (REAS-) RES ASSOC BIOTECHNOLOGY
            09-MAY-2003; 2003JP-00131392
 21-JAN-2003; 2003JP-00102206
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (first entry)
                                                                                                                                                                                                                                                                                                                                sequence of the invention
                                                                                                                                                                                                                                                                                                                                                                                                                 Conservative
                                                                   Isogai T, Sugiyama T,
Yamamoto J, Isono Y,
                                                                                                        WPI; 2004-535376/52.
                                                                                                                                                                                                                                                                                                                                                                                                 Local Similarity
les 352; Conserv
                                                                                                                      N-PSDB; ADQ63502
                                                                                                                                                                                                                                                                                                                                                           Sequence 494 AA;
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AMILIOTO-AAH19250 represent CDNAs corresponding to 27 human secreted protein genes, and AAG62136-AAG62231 represent the protein fragments. The genes and their corresponding secreted protein fragments. The genes and their corresponding secreted proteins are useful for preventing. Treating or ameliorating medical conditions, e.g., by protein or gene therapy. Pathological conditions can be diagnosed by determining the amount of the new protein in a sample or by determining the presence of mutations in the new genes. Specific uses are described for each of the 25 genes, based on the tissues in which they are most highly expressed, and include developing products for the diagnosis or treatment of 25 genes, based on the tissues in which they are most highly expressed, abnormalities, haematopoietic disorders, diseases of the immune system, abnormalities, haematopoietic disorders, diseases of the immune system, allergies, neurological disorders, e.g., Alzheimer's disease.

AIDS, autoimmune diseases (e.g., rheumatoid arthritis), inflammation, allergies, neurological disorders, e.g., Alzheimer's disease.

AIDS, autoimmune diseases, constrive disorders, schizophrenia, asthma, skin disorders and information disorders, and infections. The proteins can also be used to aid wound the cardiovascular disorders, angiogenic disorders, endecrine, construction organs before transplantation, for supporting cell culture of primary tissues, to regenerate tissues, to identify their counture of primary tissues, to regenerate tissues, to identify their counture of primary tissues, to regenerate tissues, to identify their counture of primary tissues, to regenerate tissues, to identify their controlled above, and in diagnostic immunoassays e.g., radioimmunosassay or enzyme linked immunosabent assay (ELISA). The present sequence represents a human of the invention of the invention of the invention of invention of the invention of the invention of the invention of the invention of invention of the invention of the invention of the invention o
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Novel 27 isolated human secreted proteins and polynucleotides encoding them useful for treating, diagnosing, preventing Alzheimer's disease, Parkinson's disease, AIDS, rheumatoid arthritis, asthma.
                                          gastrointestinal disorder; pregnancy-related disorder; tumour;
endocrine disorder; infection; wound healing; vulnerary; cell culture;
chemotaxis; food additive; expression; binding partner identification.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               143 ASPTSPKVFPLSLCSTOPDGNVVIACLVOGFFPOEPLSVTWSESGOGVTARNFPPSODAS
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cardiovascular disorder; anglogenic disorder; kidney disorder;
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Pred. No. 2.9e-119;
0; Mismatches 1;
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30-JUN-2000; 2000US-0215131P.
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Best Local Similarity 99.7%;
Matches 352; Conservative
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                                                                                                                                                                                                                            Homo sapiens
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The present invention relates to albumin fusion proteins comprising a therapeutic protein X and human albumin (HA, also known as human serum albumin, HSA). The proteins are useful for treating a disease or disorder that may be modulated by therapeutic protein X. The albumin extends the shelf-life of protein X, and may increase its biological in vitro/in vivo activity. The protein is useful for treating and diagnosing disorders such as cancer, reproductive disorders, disestive disorders (e.g. Crohn's such as cancer, reproductive disorders (e.g. acquired immunodeficiency syndrome, AIDS), endocrine disorders (e.g. diabetes), heamaropojetic disorders, neural disorders (e.g. Alzheimer's, Parkinson's, Creutzfeldt-Jacob disease, encephalomyelitis, meningtis, schizophrenia), and connective disorders (e.g. osteoporosis, arthritis). ABG631326-ABG65518 represent albumin fusion proteins of the invention
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SCCHPRISIHRPALEDILLGSEANLTCTLTGLRDASGVTFTWTPSSGKSAVQGPPDRDLC 180
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                                                                                                    323 GCYSVSSVLPGCAEPWNHGKTFTCTAAYPESKTPLTATLSKSGNTFRPEVHLLPPPSEEL
                    263 SCCHPRLSLHRPALEDLLLGSEANLTCTLTGLRDASGVTFTWTPSSGKSAVQGPPDRDLC
                                                                                                                                                                            383 ALNELVILTCLARGFSPKDVLVRWLQGSQELPREKYLTWASRQEPSQGTTTFAVTSILRV
                                                                            GCYSVSSVLSGCAEPWNHGKTFTCTAAYPESKTPLTATLSKSGNTFRPEVHLLPPPSEEL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Albumin fusion protein; therapeutic protein X; human albumin; HA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        human serum albumin; HSA; cancer; reproductive disorder; digestive disorder; immune disorder; endocrine disorder; haematopoietic disorder; neural disorder; connective disorder; cytostatic; antiinfertility; antiinflammatory; antiulcer; immunomodulator; anti-HIV; antidiabetic; haemostatic; nootropic; neuroprotective; antiparkinsonian; antimicrobial; neuroleptic;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Human albumin fusion protein #230.
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25-APR-2000; 2000US-0199384P.
21-DEC-2000; 2000US-0256931P.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              osteopathic; antiarthritic.
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Synthetic.
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                                                                                                                                                                                                                                                                                                                            323 GCYSVSSVLPGCAEPWNHGKTFTCTAAYPESKTPLTATLSKSGNTFRPEVHLLPPPSEEL
                                                                                                                                   143 ASPTSPKVFPLSLCSTQPDGNVVIACLVQGFFPQEPLSVTWSESGQGVTARNFPPSQDAS
                                                                                                                1 ASPTSPKVFPLSLCSTQPDGNVVIACLVQGFFPQEPLSVTWSESGQGVTARNFPPSQDAS
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                                               Length 495;
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                                               Score 1893; DB 5;
Pred. No. 2.9e-119;
                                     99.7%; Score 1.99.7%; Pred. No. 2.9e-1
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25-APR-2000; 2000US-0199384P.
21-DEC-2000; 2000US-0256931P.
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                                                             Best Local Similarity 99.7
Matches 352; Conservative
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(HASE/) HASELTINE W A.
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                 Sequence 495 AA,
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the internation features to a movel abunant huston procesh the and procesh and a parameterizal carrier; a kit comprising the albumin fusion procesh and a parameterizal carrier; a kit comprising the composition of the and a parameterizal carrier; a kit comprising the composition of the and a parameterizal carrier; a kit comprising the composition of the and subnant fusion protein; a method of treating a patient with a disease or disorder that is modulated by Therapeutic protein; x, or its fragment or variant; a method of treating a patient with a disease or disorder that is modulated by Therapeutic protein; x, or its fragment or variant; a method of extending the shelf life of Therapeutic protein, x, or its fragment or variant; a method of extending the shelf life of Therapeutic protein; x, or its fragment or variant; and the patient of the albumin fusion protein. The albumin fusion protein of the albumin fusion protein. The albumin fusion protein and its compositions have the following comprising the nuclaic adid molecule of the albumin fusion protein. The albumin fusion protein and its compositions have the following a cutylines: cytostacic, antillapsenic, manipulated, antilarchythmic, cardiant, mootropic, antilipsenic, manipulatory, immunoadulator, antilarchythmic, cardiant, mootropic, antilipsenic, manipulatory, immunoadulator, antilarchythmic, cardiant, mootropic, antilipsenic, manipulatory, manipulatory, and vulnerary. The albumin fusion protein is useful for diagnosing, treating, manipulater, antilarchythmic, cardiant and vulnerary. The albumin fusion protein in useful for diagnosing, treating, manipulater, judgines or albumin fusion or haematopoleic diseases (e.g. anamenia, Hodgkin's disease, computational anament, militar and colon, bowel disease, proteintital, indiant or language in eprocedutive system diseases (e.g. giant cell lumours), and cardiac arrest, heat valve diseases (e.g. giant cell altumours), and cardiac arrest, heat valve diseases (e.g. district and disease, partitions or real diseases or The invention relates to a novel albumin fusion protein. The invention Disclosure; SEQ ID NO 302; 279pp; English. dowloaded from the USPTO website.

1 ASPTSPKVFPLSLCSTQPDGNVVIACLVQGFFPQEPLSVTWSESGQGVTARNFPPSQDAS 99.7%; Score 1893; DB 8; Length 495; 99.7%; Pred. No. 2.9e-119; ive 0; Mismatches 1; Indels (Query Match Best Local Similarity 99.77 Matches 352, Conservative Sequence 495 AA; 143 ద à ò

Gaps ; 0

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GCYSVSVLPGCAEPWNHGKTFTCTAAYPESKTPLTATLSKSGNTFRPEVHLLPPPSEEL 382

241 ALNELVILICLARGFSPKDVLVRWLQGSQELPREKYLIWASRQEPSQGITIFAVISILRV 300

383 ALNELVILICIARGESPKDVLVRWLQGSQELPREKYLTWASRQEPSQGTTTFAVTSILRV 442 443 AAEDWKKGDTFSCMVGHEALPLAFTQKTIDRLAGKPTHVNVSVVMAEVDGTCY 301 AAEDWKKGDTFSCMVGHEALPLAFTQKTIDRLAGKPTHVNVSVVMAEVDGTCY ò g

ADR08452

ADR08452 standard; protein; 496 AA

ADR08452;

(first entry) 04 - NOV - 2004

Human protein useful for treating neurological disease Seq 1958.

human; oligo-capping method; diagnostic marker; gene therapy; osteoporosis; neurological disease; Alzheimer's disease; Parkinson's disease; dementia; short memory; cancer; sense or motor function; emotional reaction; fear response; panic; osteopathic; neuroprotective; nootropic; antiparkinsonian; cytostatic; tranquiliser

Homo sapiens

EP1447413-A2

18-AUG-2004.

12-FEB-2004; 2004EP-00003145.

14-FEB-2003; 2003JP-00102207. 09-MAY-2003; 2003JP-00131452.

(REAS-) RES ASSOC BIOTECHNOLOGY

Otsuki T; Nishikawa T, Isono Y, Sugiyama T, Nagai K, Irie R; Isogai T, Yamamoto J, Wakamatsu A, Ishii S, Isogai T,

WPI; 2004-583265/57 N-PSDB; ADR06496 New 1995 cDNA, useful for treating osteoporosis, neurological diseases, Alzheimer's diseases, Parkinson's diseases, dementia and various cancers.

Claim 1; SEQ ID NO 1958; 2686pp; English.

molecules and the encoded proteins thereof. Specifically, it refers to CDNA clones obtained by an oligo-capping method, where none of these clones are identical to any known human mRNAs. The present invention describes an immunoassay to identify agonists and antagonists, as well as antibodies, antisense molecules and siRNAs that can all be used to bind to and modulate expression of the CDNA molecules. As such, these molecules are useful for diagnostic markers or therapeutic targets for the various diseases or morbid states. In particular, they are useful in gene therapy for treating osteoporosis, meurological disease, Alzheimer's disease, Parkinson's disease, short memory and various cancers, as well as for maintaining equilibrium of sense or motor function, and for treating emotional reaction, fear response and panic. Accordingly, they exhibit osteopathic, neuroprotective, nootropic, antiparkinsonian, cytostatic and tranquiliser activities. This polypeptide is a protein encoded by a full length human cDNA sequence of the invention. NOTE: This sequence is not given in the sequence listing of the specification but can be obtained on CD-ROM from the European Patent Office, Vienna Sub-This invention relates to novel, isolated full length human cDNA

Sequence 496 AA;

Score 1893; DB 8; Length 496; Pred. No. 2.9e-119; 99.78; Query Match Best Local Similarity

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cell regeneration; membrane protein; signal transduction-related protein;
transcription-related protein; osteoporosis; neurological disease;
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R, Tamechika
                                                                                                                                                                       264 SCCHPRISIHRPALEDLIIGSEANLTCTLTGLRDASGVTFTWTPSSGKSAVQGPPDRDLC
                                               144 ASPTSPKVFPLSLCSTQPDGNVVIACLVQGFFPQEPLSVTWSESGQGVTARNFPPSQDAS
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Hio Y, Otsuka K, Nagai K, Irie
Otsuka M, Nagahari K, Masuho Y;
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(REAS-) RES ASSOC BIOTECHNOLOGY.
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25-JAN-2002; 2002US-00350978.
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352; Conservative
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Seki N, Yoshikawa T,
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N-PSDB; ADB63649.
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of the polynucleotide, immunologically assaying the polypeptide or peptide with the antibody of the encoded protein, and observing the binding between the two, a transformant carrying the polynucleotide in an expressible manner and an antisense polynucleotide. The oligonucleotide is useful as a primer for synthesising the polynucleotide. The oligonucleotide or detecting the polynucleotide. The polynucleotide, or as a probe for detecting the polynucleotide. The polynucleotides and encoded proteins are useful as pharmaceutical agents and many disease-related genes may be included in them, for developing a diagnostic marker or medicines for regulation of their expression and activity, or as targets of gene therapy. The genes are involved in tissue and/or cell respectation. Membrane proteins, signal transduction-related proteins, transcription-related proteins, signal transduction-related proteins, cranscription-related proteins, disease-related proteins and genes encoding them can be used as indicators for diseases (e.g. osteoporosis, neurological diseases, cancer, tumourer. The cDNA may be used to regulate the activity or expression of the encoded protein to treat diseases. The sequence date for this patent is not represented in the printed specification, but is based on sequence information supplied by the European Patent Office.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                             99.7%; Score 1893; DB 7; Length 497; 99.7%; Pred. No. 3e-119; ive 0; Mismatches 1; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 497 AA;
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ADQ67021
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(REAS-) RES ASSOC BIOTECHNOLOGY
                                                                            22-MAR-2002; 2002JP-00137785.
                                                    12-APR-2002; 2002EP-00008400
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                                                                                                                                                                                            N-PSDB; ADM01900
                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 508 AA;
  EP1347046-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            22-FEB-2002
                                                                                                                                             (amamoto J,
                                                                                                                             Isogai T,
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                                                                                                                                                                                                                            The invention relates to 2495 novel polynucleotides (I) and their encoded polypeptides, sequences hybridizing to these nucleotides, sequences encoding partial polypeptides and sequences having 70% to 90% identity to the nucleotide and protein sequences. The nucleotides and polypeptides are useful as diagnostic markers or therapeutic target for the diseases or morbid states. They are also useful for treating osteopromis, neurological diseases, Alzheimer's diseases, Parkinson's diseases, dementia and various cancers. This sequence corresponds to a protein
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                  204
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SCCHPRISLHRPALEDLILGSEANLTCTLTGLRDASGVTFTWTPSSGKSAVQGPPDRDLC 324
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                                                                                                                                                                 Novel 2495 cDNA, useful for treating osteoporosis, neurological diseases, Alzheimer's diseases, Parkinson's diseases, dementia and various cancers.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   241 ALNELVTLTCLARGFSPKDVLVRWLQGSQELPREKYLTWASRQEPSQGTTTFAVTSILRV 300
                                                                                                                                                                                                                                                                                                                                                                                                                                                          ASPTSPKVFPLSLCSTQPDGNVVIACLVQGFFPQEPLSVTWSESGQGVTARNFPPSQDAS
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                                                                                        Wakamatsu A, Sato H, Ishii S;
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                                                                                                                                                                                                                                                                                                                                                                                      Score 1893; DB 8; Length 497;
Pred. No. 3e-119;
0; Mismatches 1; Indels (
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                                                                                                                                                                                                        Claim 1; SEQ ID NO 4182; 2449pp; English.
                                                                                     Otsuki T, Wakam
Nagai K, Irie R;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ADM04343 standard; protein; 508
                                                             (REAS-) RES ASSOC BIOTECHNOLOGY
                        21-JAN-2003; 2003JP-00102206.
09-MAY-2003; 2003JP-00131392.
                                                                                                                                                                                                                                                                                                                                                                                         99.7%;
 21-JAN-2004; 2004EP-00001196
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                                                                                                                                                                                                                                                                                                                                      sequence of the invention
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                                                                                      Isogai T, Sugiyama T,
ramamoto J, Isono Y,
                                                                                                                            2004-535376/52.
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Best Local Similarity
Matches 352; Conserv
                                                                                                                                        N-PSDB; ADQ64833
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ADM04343
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336 GCYSVSSVLPGCAEPWNHGKTFTCTAAYPESKTPLTATLSKSGNTFRPEVHLLPPPSEEL 395
    Ishii S;
, Tamechika I;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    The invention relates to a novel human polynucleotide and the encoded polypeptide. A polynucleotide of the invention may have a use in gene therapy. An oligonucleotide of the invention ADM06202-ADM06773 is useful as a primer for synthesizing the polynucleotide or as a probe for detecting the polynucleotide. The polynucleotides ADM01316-ADM03758 are useful in gene therapy, for developing a diagnostic marker or medicines for regulating their expression and activity, or as a target of gene therapy. The proteins ADM013759-ADM06201 encoded by the polynucleotides are useful as pharmaceutical agents. The present sequence represents a protein sequence of the invention.
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                                                                                                                                                                                                                                                                                   New polynucleotides and polypeptides are useful in gene therapy, developing a diagnostic marker or medicines for regulating their expression and activity, or as a target of gene therapy.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         99.7%; Score 1893; DB 7; Length 508; 99.7%; Pred. No. 3e-119; ive 0; Mismatches 1; Indels (
Otsuki T, Wakamatsu A, Sato H, Is
Hio Y, Otsuka K, Nagai K, Irie R,
Otsuka M, Nagahari K, Masuho Y;
                                                                                                                                                                                                                                                                                                                                                                                                                                             Claim 1; SEQ ID NO 3028; 305pp; English.
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Matches 352, Conservative
r, Sugiyama T, o J, Isono Y, I
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The invention relates to an immunoadhesin comprising: (a) a chimeric intercellular adhesion molecule (ICAM)-1 comprising a rhinovirus receptor protein linked to at least a portion of an immunoglobulin heavy chain, and (b) optionally a J chain and secretory component associated with the cand (b) optionally a J chain and secretory component associated with the immunoadhesin has plant-specific glycosylation and virucide activity. The immunoadhesin is useful for reducing infection by human rhinovirus (HRV) and hence the intelation or spread of the common cold by HRV. The immunoadhesin binds to HRV and reducing infectionly, competing with call surface ICAM-1 for binding sites, interfering with virus entry or uncoating and directing premature classe of viral RNA and formation of empty capsids. Expression of the immunoadhesin having multiple binding sites have a higher effective affinity for the virus, thereby increasing the effectiveness of the immunoadhesin. Association of secretory component and immunoglobulin J chain increases the stability of the immunoadhesin in the mucosal conviconment. Production is significantly less expensive in plants than in animal cell culture and production in plants is safer for human use, since plants are not known to harbor any animal viruses. The present conviconment is that of a human immunoglobulin protein sequence, useful to
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Immunoadhesin for treating human rhinovirus infection comprises chimeric intercellular adhesion molecule-1, and optionally a J chain and secretory
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                                      Human; immunoadhesin; intercellular adhesion molecule; ICAM-1; human rhinovirus; immunoglobulin heavy chain; J chain; HRV; common cold;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 ASPTSPKVFPLSLCSTQPDGNVVIACLVQGFFPQEPLSVTWSESGQGVTARNFPPSQDAS
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Human Ig-alphal heavy chain constant region amino acid sequence
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Pred. No. 3.7e-119;
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                                                                                                                                                                                                                                                                                                                                           (PLAN-) PLANET BIOTECHNOLOGY INC.
                                                                                                                                                                                                                                                      28-APR-2001; 2001WO-US013932
                                                                                                                                                                                                                                                                                                28-APR-2000; 2000US-0200298P
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ilarity 99.4%;
Conservative
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                                                                                                                                                                                                                                                                                                                                                                                     Wycoff KL;
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Best Local Similarity
Matches 351; Conserv
                                                                                  transgenic plant.
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                                                                                                                                                                   WO200183529-A2
                                                                                                                           Homo sapiens.
                                                                                                                                                                                                             08-NOV-2001
                                                                                                                                                                                                                                                                                                                                                                                       Larrick JW,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     61 GDLYTTSSQLTLPATQCLAGKSVTCHVKHYTNPSQDVTVPCPVPSTPPTPSPSTPPTPSP 120
                   241 AINBLVTLTCLARGFSPKDVLVRWLQGSQELPREKYLTWASRQEPSQGTTTFAVTSILRV 300
241 ALNELVTLTCLARGFSPKDVLVRWLQGSQELPREKYLTWASRQEPSQGTTTFAVTSILRV 300
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                The invention relates to a novel immunoadhesin comprising a chimeric toxin receptor protein consisting of a toxin receptor protein linked to at least a portion of an immunoglobulin heavy chain with a J (joining) chain and secretory component (SC) associated with the chimeric toxin receptor protein. The immunoadhesin comprises a chimeric bacterial or viral toxin receptor protein and the immunoadhesin has plant-specific glycosylation. The immunoadhesin of the invention demonstrates virucide and antibacterial activities and may be useful for reducing the binding of a viral or bacterial antigen to a host cell and thus for treating or preventing anthrax, as well as human rhinovirus infection which results in the common cold. The current sequence is that of the human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 ASPISPKVFPLSLCSTQPDGNVVIACLVQGFFPQEPLSVTWSESGQGVTARNFPPSQDAS
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                                                                                                                                                                                                                                                                                                                                                    immunoadhesin; immunoglobulin heavy chain; J chain; joining; toxin; virucide; antibacterial; anthrax; rhinovirus infection; common cold; intercellular adhesion molecule; ICAM-1; human; constant region; IgA.
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                                                                                                                                                                                                                                                                                                                     Human IgAl heavy chain constant region protein - SEQ ID 16.
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99.4%; Pred. No. 3.7e-119;
ive 1; Mismatches 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              immunoadhesion-related protein of the invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Disclosure; SEQ ID NO 16; 288pp; English.
                                                                                                                                                                                                      AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (PLAN-) PLANET BIOTECHNOLOGY INC.
                                                                                                                                                                                                      ADE97347 standard; protein; 353
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             25-OCT-2002; 2002WO-US034197.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  26-OCT-2001; 2001US-00047542.
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N-PSDB; ADE97346, ADE97374.
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Best Local Similarity 99.4<sup>3</sup>
Matches 351; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Larrick JW, Wycoff KL;
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                                                                                                                                                                 RESULT 12
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This sequence represents the protein encoded by a cancer-suppressor gene, which is down regulated in large intestine cancer. The gene is located on chromosome 14q22. The invention also relates to a vector comprising the gene, a host cell transformed by the vector, and a process for culturing the host cell and recovering the expression product. The gene, encoded polypeptide and antibody are used in the diagnosis and treatment of cancers particularly large intestine cancer
                                                                                                              181 GCYSVSSVLPGCAEPWNHGKTFTCTAAYPESKTPLTATLSKSGNTFRPEVHLLPPPSEEL 240
                                                                                                                                                                                    241 ALNELVTLTCLARGESPKDVLVRWLQGSQELPREKYLTWASRQEPSQGTTTFAVTSILRV 300
                                                                                                                                                               241 ALNELVTLTCLARGFSPKDVLVRWLQGSQELPREKYLTWASRQEPSQGTTTFAVTSILRV 300
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Cancer-suppressor gene down-regulated in large intestine cancer, located in human chromosome 14q32, useful for diagnosis and treatment of tumors particularly large intestine cancer.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           91
                                                                                          181 GCYSVSSVLSGCAEPWNHGKTFTCTAAYPESKTPLTATLSKSGNTFRPEVHLLPPPSEEL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              32 ASPISPKVFPLSLCSTQPDGNVVIACLVQGFFPQEPLSVTWSESGGGVIARNFPPSQDAS
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                                                                                                                                                                                                                                       353
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Cancer suppressor gene; large intestine cancer; treatment; tumour;
                                                                                                                                                                                                                                   301 AAEDWKKGDTFSCMVGHEALPLAFTQKTIDRLAGKPTHVNVSVVMAEVDGTCY
                                                                                                                                                                                                                                                      301 AAEDWKKGDIFSCMVGHEALPLAFIQKTIDRLAGKPTHVNVSVVMAEVDGTCY
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                                                                                                                                                                                                                                                                                                                                                             AAY88483 standard; protein; 384
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Cancer suppressor gene product.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           chromosome 14q32.
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Matches 351;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 New immunoglobulin A polypeptide and encoding nucleic acid molecule, useful for diagnosing diabetic retinopathy using an immunologic method.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      The present invention relates to an immunoglobulin A polypeptide for diagnosing diabetic retinopathy. The composition and method are useful for diagnosing diabetic retinopathy. The present sequence represents immunoglobulin A heavy chain.
                                                                                                                                                                                                                       SCCHPRISLHRPALEDLILGSEANLTCTLTGLRDASGVTFTWTPSSGKSAVQGPPDRDLC
                                                                               GCYSVSSVLSGCAEPWNHGKTFTCTAAYPESKTPLTATLSKSGNTFRPEVHLLPPPSEEL
                                                                                                                                               181 GCYSVSSVLPGCAEPWNHGKTFTCTAAXPESKTPLTATLSKSGNTFRPEVHLLPPPSEEL
                                                                                                                                                                                                241 ALNELVTLTCLARGFSPKDVLVRWLQGSQELPREKYLTWASRQEPSQGTTTFAVTSILRV
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immunoglobulin A heavy chain.
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Best Local Similarity 99.4 Matches 351, Conservative
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N-PSDB; ADN11997.
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Query Match
Best Local Similarity
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                                                                                         ALNELVILICLARGESPKDVLVRWLQGSQELPREKYLTWASRQEPSQGTTTFAVTSILRV 300
                                                                                                            331
                                  SCCHPRLSLHRPALEDLLLGSEANLTCTLTGLRDASGVTFTWTPSSGKSAVGPPERDLC
GDLYTTSSQLTLPATQCLAGKSVTCHVKHYTNPSQDVTVPCPVBSTPPTPSPSPSTPPTPSP
                         SCCHPRLSLHRPALEDLLLGSEANLTCTLTGLRDASGVTFTWTPSSGKSAVQGPPDRDLC
                                                          GCYSVSSVLSGCAEPWNHGKTFTCTAAYPESKTPLTATLSKSGNTFRPEVHLLPPPSEEL
                                                                          GCYSVSSVLPGCAEPWNHGKTFTCTAAYPESKTPLTATLSKSGNTFRPEVHLLPPPSEEL
                                                                                                          ALNELVILICLARGESPKDVLVRWLQGSQELPREKYLTWASRQEPSQGTTTFAVTSILRV
                                                                                                                            AAEDWKKGDTFSCMVGHEALPLAFTQKTIDRLAGKPTHVNVSVVMAEVDGTCY 353
                                                                                                                                    AAEDWKKGDTFSCMVGHEALPLAFTQKTIDRLAGKPTHVNVSVVMAEVDGTCY 384
                                                                                                                                                                                                                                                    human; NOVX; cardiomyopathy; atherosclerosis; cancer; diabetes; inflammation; autoimmune disorder; allergy; blood disorder; acquired immunodeficiancy syndrome; AIDS; obesity, asthma; immunoglobulin (Ig)A nephropathy; cirrhosis; arthritis;
                                                                                                                                                                                                                                     Human NOVX protein homologue SegID 797.
                                                                                                                                                                                                                                                                                      Alzheimer's disease; infection; str
                                                                                                                                                                                   ADI17261 standard; protein; 384 AA
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2001US-0266767P.
2001US-0266975P.
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2001US-0273046P.
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05-FEB-2001;
07-FEB-2001;
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15-FEB-2001;
26-FEB-2001;
27-FEB-2001;
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31-JAN-2001;
31-JAN-2001;
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08-FEB-2001;
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This invention relates to a novel nucleic acids, and encoded polypeptides thereof, which have properties related to the stimulation of biochemical cor physical responses in a cell, tissue, organ or organism.

Cor physicalogical responses in a cell, tissue, organ or organism.

Corpusationally, it refers to the use of biologically active fragments for diagonstic and prognostic sand furthermore in the treatment of diagonstic and prognostic says well as methods to modulate their expression using antisense oligos, riboxymes and peptide nucleic acids. The NOWX polypeptides, polymucleotides and antibodies are useful in treating or preventing NOWX-associated disorders, e.g. cardiomyopathy, atherosalerosis, cancer and diabetes. Furthermore, they may be used in treating or preventing diseases such as inflammation, autoimmune consistingly, these modisorders, alteropathy, cirrhosis, arthritis, Alzheimer's disease, infections, stroke, muscular dystrophy and dispitapsy. Accordingly, these molecules have many activities including cytostatic, cardiant, antidiflammatory, immunosuppressive, antiallergic, haemostatic, anti-HIV, antidiabetic, antiarteriosclerotic, anorectic, neuroprotective, nootropic, antiarthritic, hapatotropic, antiallergic, cellaxant and anticonvulsant. In addition, they are useful in screening casasys to identify small molecules that modulate or inhibit, for example, neurogenesis, wound healing and angiogenesis. The nucleic acids are also the macogenomics. This polypeptide is a homologue of a human NOVX protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     New NOVX polypeptides and nucleic acids, useful for preventing or treating NOVX-associated disorders, e.g. cancer, cardiomyopathy, atherosclerosis, or diabetes, and in chromosome mapping, tissue typing or
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Anderson DW, Rastelli L, Miller CE;
( Colman SD, Wolenc AR, Pena CEA;
1P, Lepley DM, Rieger DK, Burgess Ci
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                         2001US-0283083P.
2001US-0285133P.
2001US-0285749P.
2001US-0288327P.
2001US-0288504P.
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2001US-0312020P.
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2001US-0318118P.
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18-OCT-2001; 2001US-0330308P.
14-NOV-2001; 2001US-0332701P.
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2001US-0323379P.
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Furtak K, Grosse WM,
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11-APR-2001;
20-APR-2001;
20-APR-2001;
23-APR-2001;
03-MAY-2001;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               31-AUG-2001; 2
07-SEP-2001; 2
07-SEP-2001; 2
                                                                                                                                                      03-MAY-2001;
29-MAY-2001;
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28-AUG-2001;
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19-SEP-2001;
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Score 1889; DB 5; Length 384; Pred. No. 4.1e-119;

99.5%;

Matches	351; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
'n	1 ASPTSPKVFPLSLCSTQPDGNVVIACLVQGFFPQEPLSVTWSESGQGVTARNFPPSQDAS 60
дд	32 ASPISPKVFPLSLCSTQFDGNVVIACLVQGFFPQEPLSVTWSESGQGVTARNFPPSQDAS 91
γ̈́ο	61 GDLYTTSSQLTLPATQCLAGKSVTCHVKHYTNPSQDVTVPCPVPSTPPTPSPSTPPTPSP 120
Ор	92 GDLYTTSSQLTLPATQCLAGKSVTCHVKHYTNPSQDVTVPCPVPSTPPTPSPSPSTPPTPSP 151
ò	121 SCCHPRISLHRPALEDLILGSEANLTCTLTGLRDASGVTFTWTPSSGKSAVGGPDRDLC 180
qα	152 SCCHPRLSLHRPALEDLLLGSEANLTCTLTGLRDASGVTFTWTPSSGKSAVQGPPERDLC 211
٥٨	181 GCYSVSSVLSGCAEPWNHGKTFTCTAAYPESKTPLTATLSKSGNTFRPEVHLLPPPSEEL 240
qq	212 GCYSVSSVLPGCAEPWNHGKTFTCTAAYPESKTPLTATLSKSGNTFRPEVHLLPPPSEEL 271
δ	241 ALNELVTLTCLARGFSPKDVLVRWLQGSQELPREKYLTWASRQEPSQGTTTFAVTSLLRV 300
οp	272 ALNELVTLTCLARGFSPKDVLVRWLQGSQELPREKYLTWASRQEPSQGTTTFAVTSILRV 331
6	301 AAEDWKKGDTFSCMVGHEALPLAFTQKTIDRLAGKPTHVNVSVVWAEVDGTCY 353
qq	332 AAEDWKKGDIFSCMVGHEALPLAFTQKTIDRLAGKPTHVNVSVVMAEVDGTCY 384
Search com Job time :	Search completed: October 25, 2005, 11:05:49 Job time : 59.8551 secs

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Ig alpha-1 chain C ig alpha-2 chain C ig alpha chain C r regil ig mu chain C r regil
                                                                                                                                        October 25, 2005, 10:59:42 ; Search time 12.158 Seconds (without alignments) 2793.604 Million cell updates/sec
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                                                                                                                                                                                                                                                                                             1 ASPTSPKVFPLSLCSTQPDG......GKPTHVNVSVVMAEVDGTCY 353
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Description
GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.
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	27.8 458 1 MHRB Ig m	27.7 452 1 MHHU 1g m	27.3 457 2 S03961 Ig m	27.3 592 2 S25705	27.0 448 2 SO3186 Ig h	26.4 391 1 MHHUBT 19 m	25.8 454 2 A46532	25.7 343 2 S25644 Ig m	.5 25.1 476 1 MHMSM Ig mu chain C regi	24.9 450 1 MHDG I9 mi	24.7 474 2 S15590 Ig h	24.7 627 2 S14683 Ig mi	24.6 479 1 MHRBM Ig mi	24.1 473 1 MHHUM IG m	23.5 328 2 147161 Ig g
1	528.5	526.5	518.5	518	512	501	490.5	488	475.5	473.5	469.5	469	466.5	458	445.5

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A, Accession: A2224

A, Mocleaule type: protein

A, Rocession: A2224

A, Mocleaule type: protein

A, Rocession: A2224

A, Note: this is the final paper in a series

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A, Altered C, P. Pysiol. Chem. 356, 1337-1342, 1975

A, Title: The primary structure of a monoclonal 1893im

A, Rocession: A9166

A, Rocession: A9166

A, Rosidues: 1-16, 72, 18, 18, 122-134, 70, 285-289, 18, 291-301, 18, 53-56, 788, 59-61, 18, 63-63, 70, 70, 235-239, 18, 720, 18, 730-353 ckRa>

A, Fitle: The covalent in Rage of secretory component to 1gA. Structure of s1gA.

A, Rocession: 83879

A, Rocession: B, Rocession: A9164, MUID: 94121784; PMID: 92226

A, Rocession: B, Contents: A9164, MUID: 94121744; PMID: 39567

A, Rocession: B, Rocession: A9164, MUID: 94121744; PMID: 39567

A, Rocession: Bostion: To, disulfide bonds

A, Rocession: Contents: A9164, MUID: 94101414; PMID: 7506257

A, Rocession: Contents: A9164, MUID: 94101414; PMID: 7506257

A, Rocession: B53110; MUID: 9410241; PMID: 7506257

A, Rocession: B53110; MUID: 9410341; PMID: 7506257
                                                                                                                                                                                                  Ig alpha-1 chain C region - human
C;Species: Homo sapiens (man)
C;Species: Homo sapiens (man)
C;Accession: A22360; A92249; A91662; S38979; B53110; A02171
R;Flanagan, J.G.; Lefranc, M.P.; Rabbitts, T.H.
Cell 36, 681-688; 1984
A;Title: Mechanisms of divergence and convergence of the human immunoglobulin alpha-1 and A;Reference number: A94653; MUID:84130179; PMID:6421489
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A,Cross-references: UNIPROT:P01876
R;Putnam, F. W.; Liu, Y.S.V.; Low, T.L.K.
J. Biol. Chem. 254, 2865-2874, 1979
A;Title: Primary structure of a human IgAl immunoglobulin. IV. Streptococcal IgAl proteast A,Reference number: A92249; MUID:79151016; PMID:107164
A;Contents: myeloma protein Bur; disulfide bonds
ALIGNMENTS
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A;Residues: 1-353 <FLA>
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Indels

Score 1838; DB 2; Pred. No. 3.2e-103; 4; Mismatches 7;

Length 352;

19 09 121

180

241

181

240

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DLYTTSSQLTLPATQCPDGKSVTCHVNHYTNPSQDVTVPCRVPSTPPTPSPFPSPF 120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           121 CCHPRISLHRPALEDLILGSEANLTCTLTGLRDASGVTFTWTPSSGKSAVEGPPERDLCG
                                                                                                                                                                                                                                                                                                                                                   DLYTTSSOLTLPATOCLAGKSVTCHVKHYTNPSODVTVPCPVPSTPPTPSPSTPPTPSPS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   LNELVTLTCLARGESPKDVLVRWLQGSQELPREKYLTWASRQEPSQGTTTFAVTSILRVA
                                                                                                                                                                                                                                                                         SPISPKVFPLSLCSIQPDGDVVVACLVQGFFPQEPLSVIWSESGQGVIARNFPPSQDASG
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                                                                                                                                                                                                       SPTSPKVFPLSLCSTQPDGNVVIACLVQGFFPQEPLSVTWSESGQGVTARNFPPSQDASG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      302 AEDWKKGDTFSCMVGHEALPLAFTOKTIDRLAGKPTHVNVSVVMAEVDGTCY 353
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 301 AEDWKKGDTFSCMVGHEALPLAFTQKTIDRLAGKPTHVNVSVVMAEVDGTCY 352
                                              96.8%;
                                       Query Match
Best Local Similarity 96.9
Matches 341; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A; Molecule type: DNA
A; Residues: 1-340 <FLA>
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                                                                                                                             A; Gene Gues. Lours 11, 103 (1, 1231), 2231, 432.33
A; Map position: 14q32.33-14q32.33
A; Map position: 14q32.33-14q32.33
A; Introns: 1/1, 103 (1, 1223), 12231, 12231, 12231, 12231, 12231, 12231, 12231, 12231, 12231, 12231, 12231, 12231, 12231, 12231, 12331, 12331, 12331, 12331, 12331, 12331, 12331, 12331, 12331, 12331, 12331, 12331, 12331, 12331, 12331, 12331, 12331, 12331, 12331, 12331, 12331, 12331, 12331, 12331, 12331, 12331, 12331, 12331, 12331, 12331, 12331, 12331, 12331, 12331, 12331, 12331, 12331, 12331, 12331, 12331, 12331, 12331, 12331, 12331, 12331, 12331, 12331, 12331, 12331, 12331, 12331, 12331, 12331, 12331, 12331, 12331, 12331, 12331, 12331, 12331, 12331, 12331, 12331, 12331, 12331, 12331, 12331, 12331, 12331, 12331, 12331, 12331, 12331, 12331, 12331, 12331, 12331, 12331, 12331, 12331, 12331, 12331, 12331, 12331, 12331, 12331, 12331, 12331, 12331, 12331, 12331, 12331, 12331, 12331, 12331, 12331, 12331, 12331, 12331, 12331, 12331, 12331, 12331, 12331, 12331, 12331, 12331, 12331, 12331, 12331, 12331, 12331, 12331, 12331, 12331, 12331, 12331, 12331, 12331, 12331, 12331, 12331, 12331, 12331, 12331, 12331, 12331, 12331, 12331, 12331, 12331, 12331, 12331, 12331, 12331, 12331, 12331, 12331, 12331, 12331, 12331, 12331, 12331, 12331, 12331, 12331, 12331, 12331, 12331, 12331, 12331, 12331, 12331, 12331, 12331, 12331, 12331, 12331, 12331, 12331, 12331, 12331, 12331, 12331, 12331, 12331, 12331, 12331, 12331, 12331, 12331, 12331, 12331, 12331, 12331, 12331, 12331, 12331, 12331, 12331, 12331, 12331, 12331, 12331, 12331, 12331, 12331, 12331, 12331, 12331, 12331, 12331, 12331, 12331, 12331, 12331, 12331, 12331, 12331, 12331, 12331, 12331, 12331, 12331, 12331, 12331, 12331, 12331, 12331, 12331, 12331, 12331, 12331, 12331, 12331, 12331, 12331, 12331, 12331, 12331, 12331, 12331, 12331, 12331, 12331, 12331, 12331, 12331, 12331, 12331, 12331, 12331, 12331, 12331, 12331, 12331, 12331, 12331, 12331, 12331, 12331, 12331, 12331, 12331, 12331, 12331, 12331, 12331, 12331, 12331, 12331, 12331, 12331, 12331, 12331, 12331, 12
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Molecule type: protein
Residues: 346-351,'X',353 <CAL>
                                                                                                             Gene: GDB:IGHA1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                61
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Ig alpha-2 chain C region (allotype A2m(1)) - human C;Species: Homo sapiens (man)
C;Species: Homo sapiens (man)
C;Accession: B22360
R;Flanagan, J.G.; Lefranc, M.P.; Rabbitts, T.H.
Cell 36, 681-688, 1984
A;Title: Mechanisms of divergence and convergence of the human immunoglobulin alpha-1 and A;Reference number: A94653; MUID:84130179; PMID:6421489
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               90.1%; Score 1710.5; DB 2; Length 340; 90.9%; Pred. No. 1.3e-95; ative 7; Mismatches 12; Indels 13;
                                                                                                                                                                                                                                                                                                                                            A;Cross-references: GDB:119333; OMIM:147000
A;Map position: 14q32.33-14q32.33
A;Introns: 1/1 103/1; 210/1
C;Superfamily: immunoglobulin C region; immunoglobulin homology C;Keywords: immunoglobulin
F;230-302/Domain: immunoglobulin homology <IMM>
                                                                                                                                                                                                                                                                     A;Cross-references: UNIPROT:P01877
C;Genetics:
A;Gene: GDB:IGHA2
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Best Local S
Matches 321
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C;Species; Gorilla gorilla (Indemnit)
C;Species; Gorilla gorilla (Gorilla)
C;Date: 07-Jun-1990 #sequence_revision 07-Jun-1990 #text_change 23-Jul-1999
C;Date: 07-Jun-1990 #sequence_revision 07-Jun-1990 #text_change 23-Jul-1999
C;Accession: S05500
R;Kawamura, S.; Omoto, K.; Ueda, S.
Nucleic Acids Res. 17, 6732, 1989
A;Title: Nucleotide sequence of the gorilla immunoglobulin alpha 1 gene.
A;Reference number: S05500; MUD:89386006; PMID:2506527
A;Accession: S05500
A;Status: translation not shown
A;Molecule type: DNA
A;Residues: 1-352 «KMA»
A;Cross-references: EMBL:X15045; NID:g22900; PIDN:CAA33147.1; PID:g22901
C;Genetics:
A;Introns: 102/1; 222/1
C;Superfamily: immunoglobulin C region; immunoglobulin homology
C;Keywords: immunoglobulin homology <IMM»
F;242-314/Domain: immunoglobulin homology <IMM»

Ig alpha-1 chain C region - gorilla (fragment) C;Species: Gorilla gorilla (gorilla) C;Date: 07-Jun-1990 #sequence_revision 07-Jun-1990 #text_change 23-Jul-1999 C;Accession: S05500

RESULT 2 S05500

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us-10-644-256-3

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A;Molecule type: protein
A;Residues: 1-92, P', 94-101, P',103-278, F',280-295, D',297-325, V',327-334, V',336-340 •
A;Residues: 1-92, P', 94-101, P', 103-278, F', 280-295, D', 297-325, V',327-334, V',336-340 •
A;Note: this chain does not form a disulfide bond with the light chain
A;Note: the A2m(1) allotype appears to be a recombinant chain, being identical (except for Bur alpha-1 chain from positions 279 to 340
C;Comment: The A2m(2) allotype sequence of the myeloma protein But is shown.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AyMap position: 14g32.33-14g32.33
C;Complex: An immunoglobulin heterotetramer subunit consists of two identical light (kapp hain disulfade bonds. In some cases, such as IgA and IgM, the subunits associate into lan C;Superfamily: immunoglobulin C region; immunoglobulin homology civeramer; immunoglobulin homology c;Keywords: duplication; glycoprotein; heterotetramer; immunoglobulin homology civeramer; interchain (to light chain) #status predicted F;109,169/Disulfide bonds: interchain (to alpha chain in another subunit) #status predicted F;339/Disulfide bonds: interchain (to J chain) #status predicted
A;Note: the disulfide bond formed by Cyg-77 is unaccounted for R;Tsuzukida, Y.; Wang, C.C.; Putnam, F.W.
Proc. Natl. Acad. Sci. U.S.A. 76, 1104-1108, 1979
A;Title: Structure of the AZm (1) allotype of human IgA-a recombinant molecule. A;Reference number: A99829; MUID:79180140; PMID:286295
A;Contents: myeloma protein Lan
A;Accession: A93829
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C;Species: Sus scrofa domestica (domestic pig)
C;Species: Sus scrofa domestica (domestic pig)
C;Date: 21-Feb-1997 #sequence_revision 21-Feb-1997 #text_change 21-Jan-2000
C;Accession: I47175
ROL Immunol. 31, 633-642, 1994
A;Title: Characterization of a C alpha gene of swine.
A;Ateference number: I47175
A;Accession: I47175
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85.3%; Pred. No. 2.3e-92;
iive 24; Mismatches 15; Indels 13;
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A;Molecule type: mRNA
A;Residues: 1-342 <BRO>
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A;Gene: GDB:IGHA2
A;Cross-references: GDB:119333; OMIM:147000
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Matches 301; Conservative
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C;Species: Homo sapiens (man)
C;Date: 17-Dec-1982 #sequence_revision 17-Dec-1982 #text_change 16-Jul-1999
C;Accession, A39828; A3829; Ā02172
R;Torano, A.; Putnam, F.W.
Proc. Natl. Acad. Sci. U.S.A. 75, 966-969, 1978
A;Title: Complete amino acid sequence of the alpha2 heavy chain of a human IgA2 immunogl A;Reference number: A93828; MUID:78137069; PMID:416441
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                                                                                                                                                                                                                                                                                                                               Ig alpha-2 chain - human (fragment)
C;Species: Homo sapiens (man)
C;Date: 02-Jul-1996 #sequence_revision 02-Jul-1996 #text_change 21-Jan-2000
                                                                                                                                                                                                                                                                                                                                                                                                              Cyaccesion: 156230
RyChintalacharuwu, K.R.; Raines, M.; Morrison, S.L.
J. Immunol. 152, 1529-5304, 1994
A.Title: Divergence of human alpha-chain constant region gene sequences. A status: Divergence of human alpha-chain constant region gene sequences. A status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule Cype: DNA
A;Residues: 1-340 < RES>
A;Cross-references: GB:S71043; NID:9546798; PIDN:AAB30803.1; PID:9546799
A;Genetics:
A;Genetics:
A;Genetics:
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Matches 319; Conservative
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A; Molecule type: protein
A; Residues: 1-340 <TOR>
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                                                          MVGHEALPLAFTQKTIDRLAGKPTHVNVSVVMAEVDGTCY
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A,Residues: 1-344 <AUF>
A,Cross-references: UNIPROT: P01878
R;Robinson, E.A.; Appella, E.
J. Biol. Chem. 254, 11418-11430, 1979
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Cispecies: Cispecies: Cispecies: Homo sapiens
Cispecies: Jose (man)
Cispecies: Jose (man)
Cispecies: Mechanisms of divergence and convergence of the human immunoglobulin alpha-1 array Reference number: A94653; MUID:84130179; PMID:6421489
A; Reference number: A94653; MUID:84130179; PMID:6421489
A; Reference number: A94653; MUID:84130179; PMID:6421489
A; Rocession: Cispecies: 
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Cross-references: EMBL:U12594; NID:g555826; PIDN:AAA65943.1; PID:g555827
                                                                                                                                                                                                                                                                                   SPTSPKVFPLSLCSTQPDGNVVIACLVQGFFPQEPLSVTWSESGQGVTARNFPPSQDASG
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                                              A;Gene: IgAcalpha
C;Superfamily: immunoglobulin C region; immunoglobulin homology
F;232-304/Domain: immunoglobulin homology <IMM>
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                                                                                                                                                                   Query Match 67.2%; Score 1275.5; DB 2; Best Local Similarity 68.8%; Pred. No. 1.5e-69; Matches 243; Conservative 32; Mismatches 65;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match 58.6%; Score 1113; DB 2; Best Local Similarity 93.2%; Pred. No. 5.2e-60; Matches 205; Conservative 10; Mismatches 5;
                                                                                                                                                                                                                                                                                                                                                                                               62
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            58 ASGGRYTMSSQLTLPPAKECPAGESVKCSVQHDSNPVQELNVKC-----SEPPLP 106
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             166
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                                                                                                                                                                                                                                                                                                                                                  Ig alpha chain C region - shrew mouse C; Species: Mus pahari C; Species: Mus pahari C; Species: Mus pahari C; Accession: A45964 #sequence_revision 17-Feb-1994 #text_change 16-Jul-1999 C; Accession: A45966 R; Osborne, B.A.; Golde, T.E.; Schwartz, R.L.; Rudikoff, S. Genetics 119, 925-931, 1988 A; Title: Evolution of the IgA heavy chain gene in the genus Mus. A; Reference number: A45966; MUID:88313645; PMID:2842228 A; Accession: A45966 A; Purp: Status: preliminary A; Molecule type: DNA A; Residues: 1-342 <0SB>
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Cispecias: Muscallus (house mouse)
Cispecias: Muscallus (house mouse)
Cispecias: Malacilus (modes)
Cispecias: Malacilus (mouse)
Cispecias: Mouse (mouse)
Cispecias: 
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  107 PSTICQPSLSLQRPALEDLLLGSDASLTCTLSGLKSTEGVVFTWEPTTGKDAVQKKPVQD
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A,Note: the authors translated the codon AAC for residue 46 as Lys, ATG
C,Superfamily: immunoglobulin C region; immunoglobulin homology
C,Keywords: immunoglobulin homology
F;232-304/Pomain: immunoglobulin homology < IMM>
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58.6%; Score 1112.5; DB 2; Length
Best Local Similarity 58.7%; Pred. No. 8.6e-60;
Matches 209; Conservative 57; Mismatches 71; Indels
181 MVGHEALPLAFTQKTIDRWAGKPTHINVSVVWAEADGTCY 220
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C;Keywords: immunoglobulin
F;142-208/Domain: immunoglobulin homology <IMM>
                                                                                                      Best Local Similarity 57.1 Matches 205; Conservative
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                                                                                              A; Molecule type: protein
A; Residues: 1, 'A', 3-17, 'C', 19-66, 'S', 68-72, 'T', 74-134, 'Q', 136-140, 'D', 142-167, 'E', 169-21
A; Note: the final C-region domain is deleted from this chain
A; Note: Cye-18 may participate in the heavy-light chain bond
B; Robinson, E.A.; Appella, E.
Proc. Natl. Acad. Sci. U.S.A. 77, 4909-4913, 1980
A; Title: Complete amino acid sequence of a mouse immunoglobulin alpha chain (MOPC 511).
A; Reference number: A93857; MUID:81054880; PMID:6776528
                                                                                                                                                                                                                                                                                                                    A. Accession: A93857
A. Molecule type: protein
A. Molecule type: protein that of mouse MOPC 47A, and a genetic mechanism for A. Mote: this chain was isolated from a myeloma protein that binds phosphorylcholine
A. Note: the sequence is compared with that of mouse MOPC 47A, and a genetic mechanism for A. Mole: this chain was isolated from a myeloma protein that binds phosphorylcholine
C. Complex: An immunoglobulin heterotetramer subunit consists of two identical light (kap hain disulfide bonds. In some cases, such as IgA and IgM, the subunits associate into le C. Superfamally: immunoglobulin heterotetramer; immunoglobulin
F. Saya-306/Domain: immunoglobulin homology < IML>
F. 234-306/Domain: immunoglobulin homology < IML>
F. 254-306/Domain: immunoglobulin homology < IML>
F. 25-84, 76-100, 114-171, 138-195/Disulfide bonds: #status predicted
F. 38, 329/Binding site: carbohydrate (Ser) (covalent) #status experimental
A;Title: Amino acid sequence of a mouse myeloma immunoglobin heavy chain (MOPC 47A) with A;Reference number: A92245; MUID:80049769; PMID:115869 A;Contents: MOPC 47A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            13
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C;Species: Oryctolagus cuniculus (domestic rabbit)
C;Species: Oryctolagus cuniculus (domestic rabbit)
C;Date: 29-Jan-1993 #sequence_revision 29-Jan-1993 #text_change 16-Jul-1999
C;Accession: S09267
R;Burnett, R.C.; Hanly, W.C.; Zhai, S.K.; Knight, K.L.
EMBO J. 8, 4041-4047, 1989
A;Title: The IgA heavy-chain gene family in rabbit: cloning and sequence analysis A;Reference number: S09264; MUID:90076124; PMID:2512120
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C;Superfamily: immunoglobulin C region; immunoglobulin homology
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            83; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          56.2%; Score 1066.5; DB 58.4%; Pred. No. 4.9e-57
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nes 206; Conservative
                                                                         A; Accession: A92245
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A,Title: The Igh heavy-chain gene family in rabbit: cloning and sequence analysis of A,Reference number: S09264; MUID:90076124; PMID:2512120 A,Accession: S09269
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  61 YTTCSLLRLLAEQCPEENSVACHVEHNYDKGQHVTVPSPPECQPPTPGPSDTTTCPCPCP 120
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                                                                                                                                                                                                                                                                                         61 GDLYTTSSQLTLPATQCLAGKSVTCHVKHYTNPSQDVTVPCPV---PSTPPTPSPSTP-P 116
                                                                                                                                                                                                                                                                                                                               60 SSLYTTCSVLSLPAEQCPAGNSVACRVEH-NNKRQDLTVPCLACNKPTIEPPTKPTCPCP 118
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            241 SEELALNELVTLTCLVRGFSPKDVLVYWTNKGVNVPENSFLVWKPLPEPGQEPTTYAVTS 300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TSILRVAAEDWKKGDTFSCMVGHEALPLAFTQKTIDRLAGKPTHVNVSVVMAEVDGTCY 353
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       299 TSLLRVPAEDWNQNESYTCVVGHBGLAEHFTQKTIDRLAGKPTHVNVSVVVADVEGVCY 357
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            4 TRPILLIPLPSPILGPGEPVVIGCLIRGFFPLGPLSVTWNTSGENLT---FPPVQSATSSL 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Ig alpha chain C region - rabbit (fragment)
C;Species: Oryctolagus cuniculus (domestic rabbit)
C;Becies: Os-Jan-1993 #sequence_revision 29-Jan-1993 #text_change 16-Jul-1999
C;Accession: S09269
ERBUDGE, R.C.; Hanly, W.C.; Zhai, S.K.; Knight, K.L.
                                                                                                                                                       TSPKVFPLSL--CSTQPDGNVVIA-CLVQGFFPQEPLSVTWSESGQGVTARNFPPSQDAS
                                                                                                                                                                                             TPPIIFPLTCPGCVLKDTSATIVAGCLIRGFFFPRGPLGVTWNDNRANLT---FPPVQSAT
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A;Molecule type: DNA
A;Residues: 1-157 <BUR>
C;Superfamily: immunoglobulin C region; immunoglobulin homology
                                                                                       Indels
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                     DB 2;
                                                                                    98;
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                     Score 1035.5; DB Pred. No. 3.7e-55;
54.64; Scor. No. 3...
57.14; Pred. No. 3...
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Use of a plan chain C region - rabbit (fragment)
C;Species: Oryctolagus cuniculus (domestic rabbit)
C;Species: Oryctolagus cuniculus (domestic rabbit)
C;Species: Oryctolagus cuniculus (domestic rabbit)
C;Species: Oso274
R;Burnett, R.C.; Hanly, W.C.; Zhai, S.K.; Knight, K.L.
R;Burnett, R.C.; Hanly, W.C.; Zhai, S.K.; Knight, R.L.
R;Burnett, R.C.; Hanly, W.C.; Zhai, R.C.; Zhai,
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                                                                                                                             4 SPRLFPLIHPRCALKDTSATVIAGCLIRGFFPLGPLSVSWNASGKNVT---FPPVPSGTS
                                                                                                                                                                                                                                     DLYTTSSQLTLPATQCLAGKSVTCHVKHYTNPSQDVTVPCPVPSTPPTPSPSTP----P
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41; Mismatches 105; Indels
199; Conservative
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                                                                                                                                                                                                                                                                                   Galpha chain C region - rabbit (fragment)
C;Species: Oryctolagus cuniculus (domestic rabbit)
C;Species: Oryctolagus cuniculus (domestic rabbit)
C;Species: Oryctolagus cuniculus (domestic rabbit)
C;Date: 29-Jan-1993 #sequence_revision 29-Jan-1993 #text_change 16-Jul-1999
C;Accession: S09265
R;Burnett, R.C.; Hanly, W.C.; Zhai, S.K.; Knight, K.L.
EMBO J. 8, 4041-4047, 1989
A;Title: The IgA heavy-chain gene family in rabbit: cloning and sequence analysis of iA;Reference number: S09264; MUID:90076124; PMID:2512120
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C;Species: Oryctolagus cuniculus (domestic rabbit)

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C;Species: Oryctolagus cuniculus

C;Species: Oryctolagus cuniculus

C;Species: S09268

R;Burnett, R.C.; Hanly, W.C.; Zhai, S.K.; Knight, K.L.

EMBO J. 8, 4041-4047, 1989

A;Title: The IgA heavy-chain gene family in rabbit: cloning and sequence analysi

A;Reference number: S09264, MUID: 90076124; PMID: 2512120

A;Recession: S09268

A;Status: not compared with conceptual translation

A;Molecule type: DNA

A;Residues: 1-358 <BUR>
C;Superfamily: immunoglobulin C region; immunoglobulin homology

C;Keywords: immunoglobulin

F;248-320/Domain: immunoglobulin homology <IMM>
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                                 64 YITSSQLTLPATQCLAGKSVTCHVKHYTNPSQDVTVPCPVPSTPPTPSPSTPPT----P
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53.5%; Score 1016; DB 2; Length 3
Best Local Similarity 57.3%; Pred. No. 5.4e-54;
Matches 205; Conservative 35; Mismatches 106; Indels
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Pred. No. 3.4e-52;
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A Klausher R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,

A Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,

A Diachenko L., Marusina K., Farmer A.H., Rubin G.M., Hong L.,

A Diachenko L., Marusina K., Farmer A.H., Rubin G.M., Hong L.,

A Diachenko L., Marusina K., Farmer A.H., Rubin G.M., Hong L.,

Brownerein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,

Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,

Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,

Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,

A Richards S., Worley D.M., Sodergren E.J., Lu X., Gibbs R.A.,

Raha S., Worley K.C., Hale S., Garcia A.M., Gab K.A.,

Rahey J., Helton E., Ketreman M., Madan A., Rodrigues S., Sanchez A.,

A Mithing M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,

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Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,

A Kraywinski M.I., Sakalska U., Smailus D.E., Schnerch A., Schein J.E.,

A Generation and initial analysis of more than 15,000 full-length human

A mouse CDNA sequences."

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01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
01-JUN-2004 (TrEMBLrel. 26, Last annotation update)
MGC21165 protein.
Homo sapiens (Human).
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
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Strausberg R.;
Submitted (AR.;
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EMBL, BC05951; AAH05951.1; -
HSSP; P01876; 10W0.
InterPro; IPR007110; Ig-11ke.
InterPro; IPR003597; Ig_c1.
InterPro; IPR003597; Ig_WHC.
InterPro; IPR003597; Ig_V.
Pfam; PF00474; Ig; I.
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PROSITE; PSS0835; IG LIKE; 4.
PROSITE; PS00290; IG MC, UNKNOWN 1.
SEQUENCE 500 AA; $4154 MW; 0A$BF43F2A3CC6D9 CRC64;
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091X92
08K172
06FDB4
06FDB4
080Z17
091WP5
091X61
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EMBL, AK121346; BAG86641.1; -.
                                                                                                                                                                                                                                                                                                                          208 GDLYTTSSQLTLPATQCLAGKSVTCHVKHYTNPSQDVTVPCPVPSTPPTPSPSTPPTPSP
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Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
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99.7%; Score 1893; DB 2; Length 494;
Best Local Similarity 99.7%; Pred. No. 8.6e-112;
Matches 352; Conservative 0; Mismatches 1; Indels
       Length 500;
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InterPro; 1PR003599; Ig.
InterPro; 1PR003599; Ig.
InterPro; 1PR003006; Ig_ME.
InterPro; 1PR003006; Ig_ME.
InterPro; 1PR003006; Ig_WHC.
InterPro; 1PR00407; Ig, 1.
SMART; SM00407; IG, 1.
SMART; SM00407; IGC1; 2.
SMART; SM00407; IGC1; 2.
SMART; SM00405; IG, 1.
SMART; SM00409; IG, 1.
SMART; SM00407; IGC1; 2.
SMART; SM00409; IG, 1.
                                                                      Indels
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Score 1894; DB 2;
Pred. No. 7.5e-112;
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Matches 352; Conservative
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TISSUB-Stomach mucosa;

Inhibashi T., Kanehori K., Yosida M., Watanabe S., Ishida S., Ono Y.,

Ishibashi T., Kanehori K., Yosida M., Watanabe S., Ishida S.,

Hotuta T., Hizoka S., Muzakawa K., Takiguchi S., Kusano J.,

Matanabe M., Fujimori K., Tanai H., Ishida M., Yamashita H., Chiba Y.,

Na Suzuki Y., Hata H., Nakagawa K., Mizuno S., Morinaga M., Kawamura M.,

Sugiyama T., Irle R., Otsuki T., Sato H., Nishikawa T., Sugiyama A.,

Kawakami B., Nagai K., Isogai T., Sato H., Nishikawa T., Sugiyama A.,

Submitted (OCT-2001) to the EMBL/GenBank/DDBJ databases.

REBL, AKOS8027; BAB71633.1; -.

REBL, PRO0300110; Ig-like.

InterPro; IPR003597; Ig-ci.

RINTERPRO; IPR003596; Ig-w.

RINTERPRO; IPR003596; Ig-w.

REPRO; PRO03597; Ig-ci.

REPRO; PR0047; ig, 1.
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                                                   GDLYTTSSQLTLPATQCLAGKSVTCHVKHYTNPSQDVTVPCPVPSTPPTPSPFTPSP
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GDLYTTSSQLTLPATQCLAGKSVTCHVKHYTNPSQDVTVPCPVPSTPPTPSPTPSP
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Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo
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PROSITE; PS50835, IG LIKE; 4.
PROSITE; PS00290; IG MHC; UNKNOWN 1.
SEQUENCE 496 AA; 53532 MW; C72EE1E247C86FED CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                             096DKO;
01-DEC-2001 (TrEMBLrel. 19, Created)
01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-WAR-2004 (TrEMBLrel. 26, Last annotation update)
Hypothetical protein FLJ25298.
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SEQUENCE FROM N.A.
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MEDLINE=79151016; Pubmed=107164.
Putnam F.W., Liu Y.-S.V., Low T.L.K.;
Putnam F.W., Liu Y.-S.V., Low T.L.K.;
"Primary structure of a human 1gAl immunoglobulin. IV. Streptococcal 1gAl protease, digestion, Fab and Fc fragments, and the complete amino acid sequence of the alpha 1 heavy chain.";
J. Biol. Chem. 254:2865-2874(1979).
327 GCYSVSSVLPGCAEPWNHGKTFTCTAAYPESKTPLTATLSKSGNTFRPEVHLLDPPSSEEL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A.
MEDLINE=84130179; PubMed=6421489; DOI=10.1016/0092-8674(84)90348-9;
Flanagan J.G., Lefranc M.-P., Rabbitts T.H.;
"Mechanisms of divergence and convergence of the human immunoglobulin alpha 1 and alpha 2 constant region gene sequences.";
Cell 36:681-688(1984).
                                                                                                     GDLYTTSSQLTLPATQCLAGKSVTCHVKHYTNPSQDVTVPCPVPSTPPTPSPPTPSP
                                                                                                                                                                                                       121 SCCHPRLSLHRPALEDLLLGSEANLTCTLTGLRDASGVTFTWTPSSGKSAVQGPPDRDLC
                                                                                                                                                                                                                                                                                                            181 GCYSVSSVLSGCAEPWNHGKTFTCTAAYPESKTPLTATLSKSGNTFRPEVHLLPPPSEEL
                                                                                                                                                                                                                                                                                                                                                                                                              241 ALNELVILTCLARGFSPKDVLVRWLQGSQELPREKYLTWASRQEPSQGTTTFAVTSILRV
                                                                                                                                                                                                                                                                                                                                                                                                                                         387 ALNELVILTCLARGFSPKDVLVRWLQGSQELPREKYLTWASRQBPSQGTTTFAVTS1LRV
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Eukaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
NCBI_TaxID=9606;
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MEDLINE=76623781; PubMed=809331;
Kratzin H., Altevogt P., Ruban E., Kortt A., Staroscik K.,
Hilschmann N.;
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01-FEB-1991 (Rel. 17, Last sequence update)
25-JAN-2005 (Rel. 46, Last annotation update)
Ig alpha-1 chain C region.
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MEDLINE=91054387; PubMed=2241915;
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A Straubberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,

A Straubberg R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,

A Staperon M.S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bahar N.K.,

Hopkins R.F., Jordan H., Moore T., Mang J., Heidh F.,

B Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,

B Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,

B Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,

B Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,

B Diatchenko L., Modellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,

B Brank S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,

R Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,

Willalon D.K., Murny D.M., Sodergen B.J., Lu X., Gibbs R.A.,

Pahey J., Helton E., Retteman M., Madan A.M., Gibbs R.A.,

Blakeiley R.W., Touchman J.W., Green B.D., Dickson M.C.,

Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Buterfield Y.S.,

R Richards M.M.: Skalska U., Smailus D.E., Schnerch A., Schein J.E.,

"Generation and initial analysis of more than 15,000 full-length human
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                                                                               324 GCYSVSSVLPGCAEPWNHGKTFTCTAAYPESKTPLTATLSKSGNTFRPEVHLLPPPSEEL 383
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     264 SCCHPRLSLHRPALEDLLLGSEANLTCTLTGLRDASGVTFTWTPSSGKSAVQGPPDRDLC 323
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                                                     181 GCYSVSSVLSGCAEPWNHGKTFTCTAAYPESKTPLTATLSKSGNTFRPEVHLLPPPSEEL
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Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
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TISSUE=Blood;
MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
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TISSUB-Blood;
TISSUB-Blood;
Strausberg R.;
Submitted (JUN-2002) to the EMBL/GenBank/DDBJ databases.
EMBL; BC032249; AAH32249.1; -.
HASPP; PORT876; 10W0.
INTERPPO; IPR003397; Ig_c1.
INTERPPO; IPR003397; Ig_c1.
INTERPPO; IPR00306; Ig_WC.
INTERPPO; IPR00306; Ig_WC.
INTERPPO; IPR003507; Q1-set; Z.
PEam; PF00047; ig; 1.
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PROSITE; PS00835; IG LIKE; 4.
PROSITE; PS00290; IG MHC; UNKNOWN 1.
SEQUENCE 499 AA; 53376 MW; 93ĀSC89582054F32 CRC64;
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Last annotation update)
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Matches 352; Conservative
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Q8N5K4;
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121 SCCHPRLSLHRPALEDLLLGSEANLTCTLTGLRDASGVTFTWTPSSGKSAVQGPPERDLC 180

GCYSVSSVLSGCAEPWNHGKTFTCTAAYPESKTPLTATLSKSGNTFRPEVHLLPPPSEEL 181 GCYSVSSVLPGCAEPWNHGKTFTCTAAXPESKTPLTATLSKSGNTFRPEVHLLPPPSEEL ALNELVTLTCLARGFSPKDVLVRWLQGSQELPREKYLTWASRQEPSQGTTTFAVTSILRV

181

GDLYTTSSQLTLPATQCLAGKSVTCHVKHYTNPSQDVTVPCPVPSTPPTFSPSTPPTFSP 120

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61 GDLYTTSSQLTLPATQCLAGKSVTCHVKHYTNPSQDVTVPCPVPSTPPTPSPFTPSP SCCHPRISLHRPALEDLILGSEANLTCTLTGLRDASGVTFTWTPSSGKSAVQGPPDRDLC

1 ASPTSPKVFPLSLCSTQPDGNVVIACLVQGFFPQEPLSVTWSESGQGVTARNFPPSQDAS

241 ALNELVILITCLARGESPKDVLVRWLQGSQELPREKYLTWASRQEPSQGTTTFAVTSILRV 300

241

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        "The structure and function of human IgA.";
Biochem. J. 271:285-226(1990).
-!- FUNCTION: Ig alpha is the major immunoglobulin class in body secretions. It may serve both to defend against local infection and to prevent access of foreign antigens to the general
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Interchain (with heavy chain).
Or C-123 with C-182 (in Ref. 4).
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Ig-like 2.
Ig-like 3.
Interchain (with light chain).
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TPS -> PST (in Ref. 2).
E -> B (in Ref. 3).
P -> S (in Ref. 3).
R -> H (in Ref. 3).
H -> R (in Ref. 3).
T -> E (in Ref. 3).
T -> E (in Ref. 3).
                                                                immunològic system.
-!- SUBUNIT: Monomeric or polymeric.
-!- SIMILARITY: Contains 3 immunoglobulin-like domains.
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N-linked (GlCNAC...).
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Pred. No. 1.1e-111;
1; Mismatches 1;
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PDB; 11GA; Model; A/B=1-353.
PDB; 10M0; X-ray; A/B=122-335.
Genew; HGNC:5478; IGHAI.
H-InvDB; HIX0012029; --
MIM; 146900; --
GO; GO:0003823; F:antigen binding; NA<sup>6</sup>
GO; GO:0006555; P:immune response; NAil InterPro; IPR007110; Ig-like.
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Best Local Similarity 99.4%;
Matches 351; Conservative
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353 AA;
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AAEDWKKGDTFSCMVGHEALPLAFTQKTIDRLAGKPTHVNVSVVMAEVDGTCY 353
                AAEDWKKGDTFSCMVGHEALPLAFTQKT1DRLAGKPTHVNVSVVMAEVDGTCY 353
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Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
NCBI_TaxID=9606;
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Zheng S., Cao J., Cao W., Cai X., Geng L.;
Submitted (UNN-1998) to the EMBL/GenBank/DDBJ databases.
R HSSP, P01876; 10W0.
R InterPro; IPR001710; Ig-1ike.
R InterPro; IPR001597; Ig-21.
R InterPro; IPR001597; Ig-21.
R InterPro; IPR001597; Ig-11.
R Ffam; PF07654; C1-set; Z.
SMART; SMO0407; IG-11. 2.
R PROSITE; PS50835; IG LIKE; 3.
R PROSITE; PS50835; IG LIKE; 3.
R PROSITE; PS60839; IG-MHC; UNKNOWN 1.
                                                                                                                                                      Last sequence update)
Last annotation update)
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99.4%; Pred. No. 1.2e-111;
ive 1; Mismatches 1;
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Matches 351; Conservative
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Name=SNC73;
Homo sapiens (Human).
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272 ALNELVTLTCLARGFSPKDVLVRWLQGSQELPREKYLTWASRQEPSQGTTTFAVTSILRV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 ASPTSPKVFPLSLCSTQPDGNVVIACLVQGFFPQEPLSVTWSESGQGVTARNFPPSQDAS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A.

TISSUB=Mammary gland;

TISSUB=Mammary gland;

TISSUB=Mammary gland;

TISSUB=Mammary gland;

TISSUB A. Ota T., Nishikawa T., Hayashi K., Otsuki T., Sugiyama T. Suzuki Y., Nagai K., Sugano S., Ishii S., Kawai-Hio Y., Saito K., Yamamoto J., Wakamatsu A., Nakamura Y., Kojima S., Nagahari K., Masuho Y., Ono T., Okano K., Yoshikawa Y., Aotsuka S., Sasaki N., Hattori A., Okumura K., Iwayanagi T., Ninomiya K.;

Submitted (MAR-2002) to the EMBL/GenBank/DDBJ databases.

EMBL; AKO74651; BAC11114.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AAEDWKKGDTFSCMVGHEALPLAFTQKTIDRLAGKPTHVNVSVVMAEVDGTCY 353
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Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
                                                                         AAEDWKKGDTFSCMVGHEALPLAFTQKTIDRLAGKPTHVNVSVVMAEVDGTCY
                                             301 AAEDWKKGDTFSCMVGHEALPLAFTQKTIDRLAGKPTHVNVSVVMAEVDGTCY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match 99.5%; Score 1889; DB 2; Length 493; Best Local Similarity 99.4%; Pred. No. 1.5e-111; Matches 351; Conservative 1; Mismatches 1; Indels (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             InterPro; IRR00110; Ig-like.
InterPro; IRR00110; Ig-like.
InterPro; IRR001306; Ig-WHC.
InterPro; IRR001306; Ig-WHC.
InterPro; IRR001505; Ig-V.
Pfam; PF07654; Cl-Set; Z.
SMART; SM00406; IGV; I.
PROSITE; PS000290; IG LIKE; 4.
PROSITE; PS002090; IG MHC; UNKNOWN I.
SEQUENCE 493 AA; $53224 MW; 12ECD7E094777101 CRC64;
                                                                                                                                                                                                                                                               01-OCT-2002 (TrEMBLrel. 22, Created)
01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
01-OMR-2004 (TrEMBLrel. 26, Last annotation update)
Hypothetical protein FLJ90170.
Homo sapiens (Human).
                                                                                                                                                                                                                    493 AA.
                                                                                                                                                                                                                    PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                         NCBI_TaxID=9606;
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QGGMX2
ID QGGMJ
AC QGGMJ
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09NCL6
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01-0
01-0
01-0
01-0
01-0
01-0
02 Homo
0C Eukam
0C Bukam
0C Buka
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MEDINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;

XI TISSUB=Spleen;

XI Alusher R.D., Collins F.S., Magner L., Shenmen C.M., Schuler G.D.,

A Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,

A Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,

A Diatchenko L., Marusina K., Paren A.A., Rubin G.M., Hong L.,

A Diatchenko L., Marusina K., Paren A.A., Rubin G.M., Hong L.,

A Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,

A Raha S.S., Loquellano N.B., Peters G.J., Abramson R.D., Mullahy S.J.,

Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,

Richards S., Worley K.C., Hale S., Carcia A.M., Gay L.J., Hulyk S.W.,

A Nilalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,

Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,

Rodriguez A.C., Grimwood J., Schutz J., Myers R.M., Butterfield Y.S.,

A Dones S.J., Marra M.A.,

A Jones S.J., Marra M.A.,

"Generation and initial analysis of more than 15,000 full-length human and mouse C.D.A.
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Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
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A Strausberg R.;

Strausberg R.;

Strausberg R.;

Submitted (UNN-2004) to the EMBL/GenBank/DDBJ databases.

EMBL; BC073771; AAH77771.1; -.

R InterPro; IPR001599; Ig. 1g-1;

R InterPro; IPR001599; Ig. 21.

R InterPro; IPR001596; Ig. 40.

R InterPro; IPR001596; Ig. 40.

R Pfam; PF07654; C1.set; Z.

R Pfam; PF07654; C1.set; Z.

R SMART; SM00409; IG. 4.

R SMART; SM00409; IG. 4.

R SMART; SM00409; IG. 1.

R PROSITE; PS00290; IG. MHC; UNKNOWN_1.

R PROSITE; PS00290; IG. MHC; UNKNOWN_1.

R PROSITE; PS00290; IG. MHC; UNKNOWN_1.
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99.5%; Score 1889; DB 2; Length 4
Best Local Similarity 99.4%; Pred. No. 1.5e-111;
Matches 351; Conservative 1; Mismatches 1; Indels
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Created)
Last sequence update)
Last annotation update)
                                                                                                       Hypothetical protein.
                                                                                                                                                    (Human)
                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.
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493 AA

PRELIMINARY;

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REVIEWEE FROM N.A.

REVIEWEE TO NISHIRAWA TO CHANGE TO SUBJOURD THE R.Y.

RA CLE T. SUBLIK Y. NISHIRAWA T., OCENHI T., SUBJOURD T., ITHE R.,

RA CLE T., SUBLIK Y. NISHIRAWA T., SUBJOURD T., TADAKA T., ISHIR S.,

RA GRANDER M., Obsyashi M., Nishi T., Shibbehara T., Tanaka T., Ishir S.,

RA MURAMEN M., Obsyashi M., Kamod T., Isono Y., Nagahari K.,

RA MURAMIN M., Kanda K., Yokou T., FULLY T., Kankawa E., Omura Y.,

RA Takahashi M., Kanda K., Yokou T., FULLY T., Kikkawa E., Omura Y.,

RA Takahashi T., Yamashita H., Murakawa M., Yamazaki M.,

RINOMIYA K., Ishibashi T., Yamashita H., Murakawa K., Pijimori K.,

RA Takahashi T., Yamashita H., Murakawa K., Pijimori K.,

RA Takahashi T., Yamashita H., Murakawa K., Pijimori K.,

RA Takahashi F., Jimibashi T., Yamashi M., Hotuta T., Kusano J.,

RA Ranehori K., Takahashi F.Jiji A., Hara H., Tanasa T., Nomura Y.,

RA Kanehori K., Takahashi F.Jiji A., Takakuchi K., Arita M., Hotuta T., Kusano J.,

RA Kanehori K., Takahashi F.Jiji A., Takakuchi K., Arita M., Hotuta T., Kusano J.,

RA Kanehori K., Takahashi F.Jiji A., Takakuchi K., Arita M., Hotuta T., Kusano J.,

RA Kanehori K., Takahashi F.Jiji A., Takakuchi K., Shiohata N., Sano S.,

RA Woshikawa Y., Matsunaw H., Ichhara T., Shiohata N., Sano S.,

RA Wamazaki M., Watanabe T., Sugiyama A., Takami S., Takami B.,

RA Matsumura K., Nawakami T., Noguchi S., Itoh T., Shigeta K., Senba T.,

RA Matsumura K., Nakajama Y., Mizuno T., Morinaga M., Sasaki M.,

RA Watsumura K., Nakajama Y., Matsuho M., Komatsu T.,

RA Matsumura K., Nagaso T., Nomura N., Kikuchi H., Masuho Y., Yamashita R.,

RA Wakabata K., Nakajama Y., Ozaki K., Hirao M., Ookumura K.,

RA Matsumura K., Nagaso T., Nomura N., Kikuchi H., Masuho Y., Yamashita R.,

RA Wakabata K., Yamagano J., Satch T., Shirai Y., Takahashi Y., Nagaso T., Nawai K., Yamashita R., Nakai K., Yamashita R., Nakai K., Yamashita R., Rawakami R., Nakai K., Yamashita R., Nakai K., Yamashita R., Rawakami R., Nakai K., Yamashita R., Nakai K., Yamashita R., Romiyama M., Nakai K., Na
                                                                         440
ALNELVILITCLARGESPKDVLVRWLQGSQELPREKYLTWASRQEPSQGTTTFAVTSILRV
                                    301 AAEDWKKGDTFSCMVGHEALPLAFTQKTIDRLAGKPTHVNVSVVMAEVDGTCY 353
                                                                                                                                                                                                                                                                                                                                                                                                                                    01-DEC-2001 (TrEMBLrel. 19, Created)
01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-DEC-2004 (TrEMBLrel. 19, Last annotation update)
Hypothetical protein FLJ14473.
Homo sapiens (Human).
Homo sapiens (Homan).
Mammalia, Eutherazoa, Chordata, Craniata, Vertebrata, Euteleostomi, Mammalia, Eutheria, Primates; Catarrhini; Hominidae, Homo.
                                                                                                                                                                               441 AAEDWKKGDTFSCMVGHEALPLAFTQKTIDRLAGKPTHVNVSVVMAEVDGTCY
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EMBL; AK027379; BAB55072.1; -.

PIR, S21205; S21205.

HSSP; P01876; 10W0.

InterPro; IPR007110; Ig-like.

InterPro; IPR003597; Ig.cl.

InterPro; IPR003596; Ig.wHC.

InterPro; IPR03596; Ig.v.

Pfam; PF07654; C1-set; Z.

SMART; SM0406; IGV; 1.

PROSITE; PS06035; IG_LIKE; 4.

PROSITE; PS06035; IG_LIKE; 4.

PROSITE; PS06039; IG_MHC; UNKNOWN 1.

SEQUENCE 494 AA; $\frac{5}{2}3088 MW; 9AID7AEBSAEE4C0E CRC64;
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A Strausberg R.L., Feingold E.A., Grouse L.H., Derged J.G.,

A Strausberg R.L., Feingold E.A., Grouse L.H., Derged J.G.,

A Strausherg R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,

A Stachul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhara N.K.,

RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,

A papeleron M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,

RA Brownstein M.J., Usdin T.B., Tooshiyuki S., Carninci P., Prange C.,

RA Brownstein M.J., Usdin T.B., Tooshiyuki S., Carninci P., Prange C.,

Raba S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,

Robark S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunarane P.H.,

Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,

A Raha S.S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,

A Norley W., Peters G.J., Lu X., Glbbs R.A.,

Richards S., Worley M., Sodergren E.J., Lu X., Glbbs R.A.,

Radan A., Young A.C., Shevchenko Y., Bouffard G.G.,

Radriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,

Radriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,

Radriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,

Radriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,

Radriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,

Radriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,

Radriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,

Radriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,

Radriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,

Radriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,

Radriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield M. S.,

Radriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,

Radriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Myermon B.J., Marra M.A.,
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                                                  201
                                                                                                          GDLYTTSSQLTLPATQCLAGKSVTCHVKHYTNPSQDVTVPCPVPSTPPTPSPSTPFTPSP 120
                                                                                                                                                               261
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                                                                                                                                                                                                                                                     262 SCCHPRLSLHRPALEDLLLGSEANLTCTLTGLRDASGVTFTWTPSSGKSAVQGPPERDLC
1 ASPTSPKVFPLSLCSTQPDGNVVIACLVQGFFPQEPLSVTWSESGQGVTARNFPPSQDAS
                 202 GDLYITSSQLILPATQCLAGKSVTCHVKHYINPSQDVTVPCPVPSTPPTPSPSTPPTPSP
                                                                                                                                                                                                                       SCCHPRISLHRPALEDLILGSEANLTCTLTGLRDASGVTFTWTPSSGKSAVQGPPDRDLC
                                                                                                                                                                                                                                                                                                                                                            322 GCYSVSSVLPGCAEPWNHGKTFTCTAAYPESKTPLTATLSKSGNTFRPEVHLLPPPSEEL
                                                                                                                                                                                                                                                                                                                                                                                                                                                  241 ALNELVTLTCLARGFSPKDVLVRWLQGSQELPREKYLTWASRQEPSQGTTTFAVTSILRV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   382 ALNELVILTCLARGFSPKDVLVRWLQGSQELPREKYLTWASRQEPSQGTTTFAVTSILRV
                                                                                                                                                                                                                                                                                                                                     GCYSVSSVLSGCAEPWNHGKTFTCTAAYPESKTPLTATLSKSGNTFRPEVHLLPPPSEEL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Eukaryota, Metazoa; Chordata; Craniata; Vortebrata; Euteleostomi;
Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TISSUE=Lung;
MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Strausberg R.;
Submitted (OCT-2001) to the EMBL/GenBank/DDBJ databases.
EMBL; BCG16369; AAH16369.1; -.
HSSP; POL876; 10W0.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       096KX8;
01-DEC-2001 (TrEMBLrel. 19, Created)
01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
MGC27165 protein.
Homo sapiens (Human)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sci. U.S.A. 99:16899-16903(2002)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         InterPro, IPR007110; Ig-like
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    InterPro; IPR003597; Ig_cl.
InterPro; IPR003006; Ig_MHC.
InterPro; IPR003506; Ig_v.
Pfam: PP07654; Cl-set; Z.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    cDNA sequences."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Pfam; PF07654; C1-set;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A.
TISSUE=Lung;
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154 ASPTSPKVFPLSLCSTQPDGNVVIACLVQGFFPQEPLSVTWSESGQGVTARNFPPSQDAS 213
                                                                                                                                                                                  61 GDLYTTSSQLTLPATQCLAGKSVTCHVKHYTNPSQDVTVPCPVPSTPPTPSPSTPPTFSP 120
                                                                                                                                                                                                                                                                                                         121 SCCHPRLSLHRPALEDLLLGSEANLTCTLTGLRDASGVTFTWTPSSGKSAVQGPPDRDLC 180
                                                                                                                                                                                                                                                                                                                                         274 SCCHPRLSLHRPALEDLLLGSEANLTCTLTGLRDASGVTFTWTPSSGKSAVQGPPERDLC 333
                                                                                                                                                                                                                                                                                                                                                                                                                                                               334 GCYSVSSVLPGCAEPWNHGKTFTCTAAYPESKTPLTATLSKSGNTFRPEVHLLPPPSEEL 393
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     394 ALNELVILICIARGFSPKDVLVRWLQGSQELPREKYLTWASRQEPSQGTTTFAVTSILRV 453
                                                                                                                                                                                                                  214 GDLYTTSSQLTLPATQCLAGKSVTCHVKHYTNPSQDVTVPCPVPSTPPTPSPSTPPTPSP
                                                                                                                                                                                                                                                                                                                                                                                                                               181 GCYSVSSVLSGCAEPWNHGKTFTCTAAYPESKTPLTATLSKSGNTFRPEVHLLPPPSEEL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     241 ALNELVTLTCLARGFSPKDVLVRWLQGSQELPREKYLTWASRQEPSQGTTTFAVTSILRV
                                                         1 ASPTSPKVFPLSLCSTQPDGNVVIACLVQGFFPQEPLSVTWSESGQGVTARNFPPSQDAS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              The German Human CDNA Consortium;
Wambutt R., Heubner D., Mewes H.W., Weil B., Amid C., Osanger A.,
Fobo G., Han M., Wiemann S.;
Submitted (AUG-2003) to the EMBL/GenBank/DDBJ databases.
EMBL; BX640624; CAE45778.1; -.
HSSP; P01842; 1AQK.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             519 AA; 56423 MW; F839EE7F811EB88D CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        05-JUL-2004 (TrEMBLrel. 27, Created)
05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
Hypotetical protein DKFZp686K18196 (Fragment)
Name-DKFZp686K18196,
Homo sapiens (Human)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match 99.5%; Score 1889; DB 2; Best Local Similarity 99.7%; Pred. No. 1.6e-111; Matches 351; Conservative 0; Mismatches 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     519 AA
      1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             InterPro; IPR003599; 19.
InterPro; IPR003110; 19-like.
InterPro; IPR003100; 19-like.
InterPro; IPR003597; 19_c1.
InterPro; IPR003596; 19_WHC.
InterPro; IPR003596; 19_WHC.
InterPro; IPR0047; 21.
SMART; SM00407; 16; 4.
SMART; SM00407; 16c1; 2.
SMART; SM00407; 16c1; 2.
PR0SITE; PS00290; 1G_MHC; UNKNOWN_1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TISSUE=Human esophagus tumor;
   Matches 351; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Hypothetical protein
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Q6N092;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                               263
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            121 SCCHPRLSLHRPALEDLLLGSEANLTCTLTGLRDASGVTFTWTPSSGKSAVQGPPDRDLC 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        323
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              241 ALNELVTLTCLARGFSPKDVLVRWLQGSQELPREKYLTWASRQEPSQGTTTFAVTSILRV 300
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The German Human CDNA Consortium;

Bloecker H., Boecher M., Mewes H.W., Weil B., Amid C., Osanger A.,

Bloecker H., Boecher M., Mewes H.W., Weil B., Amid C., Osanger A.,

L. Submitted (Aug-2003) to the EMBL/GenBank/DDBJ databases.

R. BEBL; BX640847; CAE45917.1; -.

R. BEBL; BX640847; CAE45917.1; -.

R. HSPF, P01751; 1A6W.

InterPro; IPR001599; Ig.

R. InterPro; IPR001599; Ig.

R. InterPro; IPR001506; Ig.

R. InterPro; IPR003596; Ig.

R. InterPro; IPR003596; Ig.

R. RART; SM00409; IG; 4.

SWART; SM00409; IG; 4.

SWART; SM00407; IG.

R. RART; SM004007; IG.

                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1 ASPISPKVFPLSLCSTOPDGNVVIACLVQGFFPQEPLSVTWSESGQGVTARNFPPSQDAS
                                                                                                                                                                                                                                                                                                            144 ASPTSPKVFPLSLCSTQPDGNVVIACLVQGFFPQEPLSVTWSESGQGVTARNFPPSQDAS
                                                                                                                                                                                                                                                                                                                                                                                                                                     204 GDLYTTSSQLTLPATQCLAGKSVTCHVKHYTNPSQDVTVPCPVPSTPPTPSPSTPPTPSP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            384 ALNELVILICLARGESPKDVLVRWLQGSQELPREKYLTWASRQEPSQGTTTFAVTSILRV
                                                                                                                                                                                                                  Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
                                                                                                                                                                                                                  .
                                                                                                                                                  Query Match
Best Local Similarity 99.4%; Pred. No. 1.5e-111;
Matches 351; Conservative 1; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            99.5%; Score 1889; DB 2; Length 506; 99.4%; Pred. No. 1.6e-111;
SMART; SM00406; IGV; 1.
PROSITE; PS50835; IG_LIKE; 4.
PROSITE; PS00290; IG_MHC; UNKNOWN 1.
SEQUENCE 496 AA; $3391 MM; D346929849040D69 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   506 AA; 54459 MW; 1D9477A37B77C3A0 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           05-JUL-2004 (TrEMBLrel. 27, Created)
05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
Hypothetical protein DKFZp686J11235 (Fragment).
Name-DKFZp686J11235,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        506 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.
TISSUE=Human small intestine;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Appothetical protein
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                                               122 CCHPRLSLHRPALEDLLLGSEANLTCTLTGLRDASGVTFTWTPSSGKSAVQGPPDRDLCG 181
                                                                                                                                               242 LNELVTLTCLARGFSPKDVLVRWLQGSQELPREKYLTWASRQEPSQGTTTFAVTSILRVA 301
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                                                              288 CCHPRLSLHRPALEDLLLGSEANLTCTLTGLRDASGVTFTWTPSSGKSAVQGPPDRDLCG
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            228 DLYTTSSQLTLPATQCLAGKSVTCHVKHYTNPSQDVTVPCPVPSTPPTPSPSTPPTPSPS
                                                                                                                                                            154 ASPTSPKVFPLSLCSTQPDGNVV1ACLVQGFFPQEPLSVTWSESGQGVTARNPPPSQDAS
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                                                                                               182 CYSVSSVLSGCAEPWNHGKTFTCTAAYPESKTPLTATLSKSGNTFRPEVHLLPPPSEELA
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                                                                                                                                                                                                                                                                                                                                                                                                                                TISSUERNCE FROM N.A.

TISSUE-Human rectum tumor;

TISSUE-Human rectum tumor;

The German Human cDNA Consortium;

A wmbutt R., Heubner D., Mewes H.W., Weil B., Amid C., Osanger A.,

Pobo G., Han M., Wiemann S.;

Submitted (AUG-2003) to the EMBL/GenBank/DDBJ databases.

EMBL; BX640626; CG45780.1; -..

EMBL; BX640626; CG45780.1; -..

R InterPro; IPR00110; Ig-like.

InterPro; IPR001599; Ig-

InterPro; IPR001599; Ig-

InterPro; IPR001596; Ig-MHC.

R InterPro; IPR001596; Ig-MHC.

R PEAM; FR0664; C1-set; Z.

R SMART; SM00409; IG-1.

R SMART; SM00406; IG-1.

R PROSITE; PS50835; IG-LIKE; 4.

R PROSITE; PS50835; IG-LIKE; 4.

M HYDOCHELICAL Protein.
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                                                                                                                                                                                              302 AEDWKKGDTFSCMVGHEALPLAFTQKTIDRLAGKPTHVNVSVVMAEVDGTCY 353
                                                                                                                                                                                                             468 AEDWKKGDIFSCAVGHEALPLAFIQKTIDRLAGKPTHVNVSVVWAEVDGTCY 519
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Mammalia, Butheria, Primates, Catarrhini, Hominidae, Homo.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            tch 99.3%; Score 1884; DB 2; Length 506; al Similarity 99.2%; Pred. No. 3.3e-111; 350; Conservative 1; Mismatches 2; Indels
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                                                                                                                                                                                                                                                                                              Q6N090;
05-JUL-2004 (TrEMBLrel. 27, Created)
05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
Hypothetical protein DKFZp686G21220 (Fragment).
                                                                                                                                                                                                                                                                                      506 AA
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                                                                                                                                                                                                                                                                                    PRELIMINARY;
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Matches
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                        334 GCYSUPSVLPGCAEPWNHGKTFTCTAAYPESKTPLTATLSKSGNTFRPEVHLLPPPSEEL 393
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    09
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GCYSVSSVLSGCAEPWNHGKTFTCTAAYPESKTPLTATLSKSGNTFRPEVHLLPPPSEEL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            145 ASPTNPKVFPLSLCSTQPDGNVVIACLVQGFFPQEPLSVTWSESGQGVTARNFFPSQDAS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 205 GDLYITSSQLILPATQCLAGKSVTCHVKHYINPSQDVTVPCPVPSTPPTPSPSTPPTPSP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           241 ALNELVTLTCLARGFSPKDVLVRWLQGSQELPREKYLTWASRQEPSQGTTTFAVTSILRV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 ASPTSPKVFPLSLCSTQPDGNVVIACLVQGFFPQEPLSVTWSESGQGVTARNFPPSQDAS
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                                                                                                                                                                                                                                  454 AAEDWKKGDTFSCMVGHEALPLAFTQKTIDRLAGKPTHVNVSVVMAEVDGTCY 506
                                                                                                                                                                                                       AAEDWKKGDTFSCMVGHEALPLAFTQKTIDRLAGKPTHVNVSVVMAEVDGTCY 353
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Homo sapiens (Human),
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Zheng S., Shao X., Cao J., Geng L., Fang Y., Dong Q.; Submitted (JUN-2000) to the EMBL/GenBank/DDBJ databases. BMBL, Pag1866, AAL36987.1; -. HSSP; P01876; 10W0. Pfam; PF07654; C1-set; 2. SMART; SM00406; IGv; 1. PROSITE; PS050835; IG_LIKE; 4. PROSITE; PS050830; IG_MHC; UNKNOWN 1. SRQUENCE 497 AA; $3665 MW; F24D08DFA5A663E5 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      99.1%; Score 1881; DB 2; 98.9%; Pred. No. 5e-111; iive 2; Mismatches 2;
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                                                                                                                                                                                                                                                                                                                                                                                           497
                                                                                                                                                                                                                                                                                                                                                                                                                                             Created)
                                                                                                                                                                                                                                                                                                                                                                                           PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                       01-MAR-2002 (TrEMBLrel. 20, 01-MAR-2002 (TrEMBLrel. 20, 01-MAR-2004 (TrEMBLrel. 26, SNC66 protein.
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Matches 349; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         interchain (with heavy chain) (or with C-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ASPTSPKVFPLSLCSTQPDGNVVIACLVQGFFPQBPLSVTWSESGQGVTARNFPPSQDAS
                                                                                                                                                                                                                                                                                                                                                                                                        0; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Interchain (with heavy chain of another
                                                                                                                                   Kawamura S., Omoto K., Ueda S.;
"Nucleotide sequence of the gorilla immunoglobulin alpha 1 gene.";
Nucleotide sequence of the gorilla immunoglobulin class in body
'-!- FUNCTION: Ig alpha is the major immunoglobulin class in body
secretions. It may serve both to defend against local infection
and to prevent access of foreign antigens to the general
immunologic system.
-!- SIMILARITY: Contains 3 immunoglobulin-like domains.
                          Gorilla gorilla gorilla (Lowland gorilla).
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Gorilla.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     similarity).
Or C-123 with C-182 (By similarity)
By similarity.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              N-linked (GlcNAc. . .) (Potential)
N-linked (GlcNAc. . .) (Potential)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Interchain (with light chain) (By similarity).
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Pred. No. 1e-108;
4; Mismatches 7; Indels (
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Interchain (with J chain) (By
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  subunit) (By similarity).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           4820E8DB02AC7514 CRC64;
25-JAN-2005 (Rel. 46, Last annotation update)
Ig alpha-1 chain C region.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 By similarity. By similarity.
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                                                                                                                                                                                                                                                                                                                                                         EMBL; X15045; CAA33147.1; ALT_INIT.
HSSP; P01876; 10W0.
                                                                                              SEQUENCE FROM N.A.
TISSUE-Lymph node;
MEDLINE-89386006; PubMed-2506527;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         180)
                                                                                                                                                                                                                                                                                                                                                                              InterPro; IPR007110; Ig-like.
InterPro; IPR003597; Ig.cl.
InterPro; IPR003066; Ig_MHC,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           37755 MW;
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Best Local Similarity 96.94
Matches 342; Conservative
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353 AA;
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                         Name=IGHA1;
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Search completed: October 25, 2005, 11:07:53 Job time : 51.728 secs

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OTHER INFORMATION: Xaa equals
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; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
US-09-800-729-112
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OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
NAME/KEY: SITE
LOCATION: (494)
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98.4%; Score 1867; DB 4; Length 530;
Best Local Similarity 98.9%; Pred. No. 2e-143;
Matches 348; Conservative 0; Mismatches 4; Indels
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Sequence 112, Application US/09800729

Fatent No. 6605592

GENERAL INFORMATION:

APPLICANT: Ni et al.

ITILE OF INVENTION: 32 Human secreted proteins
FILE REFERENCE: PZ044P1

CURRENT APPLICATION NUMBER: US/09/800,729

CURRENT FILING DATE: 2001-03-08

PRIOR FILING DATE: 2001-09-22

PRIOR FILING DATE: 1999-09-24

NUMBER OF SEQ ID NOS: 217

SOFTWARE: Patentin Ver. 2.0

SEQ ID NO 112

LENGTH: 530

LENGTH: 530
US-09-472-087-6
US-09-472-087-64
US-09-472-087-68
US-09-472-087-68
US-09-872-087-66
US-09-859-053-32
US-09-859-053-32
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Best Local Similarity 97.5%; Pred. No. 4.6e-143;
Matches 344; Conservative 5; Mismatches 4;
                                                                                                                                                                                                                                                                                                                                           Sequence 216, Application US/09800729

Patent No. 6605592

GENERAL INFORMATION:

APPLICATION NI et al.

TITLE OF INVENTION: 32 Human secreted proteins
FILE REFERENCE: P2044P1

CURRENT APPLICATION NUMBER: US/09/800,729

CURRENT FILING DATE: 2001-03-08

PRIOR FILING DATE: 2000-09-22

PRIOR FILING DATE: 1999-09-24

NUMBER OF SEQ ID NOS: 217

SOFTWARE: Patentin Ver. 2.0

SEOFTWARE: Patentin Ver. 2.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TYPE: PRT
ORGANISM: Homo sapiens
US-09-800-729-216
                                                                                                                                                                                                                                                                                                              RESULT 2
US-09-800-729-216
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US-09-049-672A-1; Sequence 1, Application US/09049672A; Patent No. 6135941; GENERAL INFORMATION:

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                     APPLICANT: Tang, Y. Tom APPLICANT: Tang, Y. Tom APPLICANT: Yue, Henry APPLICANT: Yue, Henry APPLICANT: Yue, Henry APPLICANT: Yue, Henry APPLICANT: Au-Young, Janice APPLICANT: Guegler, Karl J. APPLICANT: Guegler, Karl J. APPLICANT: Buggin, Mariah R. TITLE OF INVENTION: Human immune system ASSOCIATED PROTEINS NUMBER OF SEQUENCES: 28 CORRESPONDENCE ADDRESS: ADDRESSE: Incyte Pharmaceuticals, Inc. STREET: 3174 Porter Drive CITY: Palo Alto STATE: CA COUNTRY: USA
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98.1%; Score 1861; DB 3;
Best Local Similarity 97.5%; Pred. No. 5.7e-143;
Matches 344; Conservative 6; Mismatches 3;
                                                                                                                                                                                                                                                                                                                                                                              COMPUTER READABLE FORM:

MEDIUM TYPE: Diskette
COMPUTER: Diskette
COMPUTER: Diskette
COMPUTER: DISKETTE
COPENATING SYSTEM: DOS
SOFTWARE: FASTSEQ for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/049,672A
FILING DATE: HEREWITH
CLASSIFICATION Si6
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
ATTORNEY,AGENT INFORMATION:
NAME: Cerrone, Michael C
REGISTRATION NUMBER:
NAME: Cerrone, Michael C
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TELECOMMUNICATION INFORMATION:
TELEPHONE: 650-855-0555
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     INFORMATION FOR SEQ ID NO: 1: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     LENGTH: 499 amino acids
TYPE: amino acid
Lal, Preeti
Tang, Y. Tom
Yue, Henry
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STRANDEDNESS: Single TOPOLOGY: linear IMMEDIATE SOURCE: LIBRARY: ADENINBO1 CLONE: 021145
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TELEFAX: 650-845-4166
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371 ALNELVILTCLARGFSPKDVLVRWLQGSQELPREKYLTWASRQEPSQGTTTFAVTSILRV 430
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                121 SCCHPRLSLHRPALEDLLLGSEANLTCTLTGLRDASGVTFTWTPSSGKSAVQGPPDRDLC 180
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                   311 GCYSVSSVLPGCAQPWNHGETFTCTAAHPELKTPLTANITKSGNTFRPEVHLLPPPSEEL 370
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  181 GCYSVSSVLSGCAEPWNHGKTFTCTAAYPESKTPLTATLSKSGNTFRPEVHLLPPPSEEL
                                                                                                                                                                    301 AAEDWKKGDTFSCMVGHEALPLAFTQKTIDRLAGKPTHVNVSVVMAEVDGTCY 353
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                                                                                                                                                                                          431 AAEDWKKGDTFSCMVGHEALPLAFTQKTIDRLAGKPTHVNVSVVMAEVDGTCY
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Patent No. 5622842;
GENERAL INFORMATION:
APPLICANT: HOLLIS, GREGORY F.
APPLICANT: HOLLIS, MAYUR D.
TITLE OF INVENTION: DNA ENCODING CANINE IMMUNOCLOBULIN;
NUMBER OF SEQUENCES: 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DB 4;
                                                                                                                                                                                                                                                                                                          Sequence 145, Application US/09800729

Patent No. 6605592

GENERAL INFORMATION:
APPLICANT: Ni et al.
TITLE OF INVENTION: 32 Human secreted proteins
FILE REFERENCE: PC144P1
CURRENT APPLICATION NUMBER: US/09/800,729
CURRENT FILING DATE: 2001-03-08
PRIOR PLILING DATE: 2000-09-22
PRIOR PLILING DATE: 1999-09-24
PRIOR FILING DATE: 1999-09-24
NUMBER OF SEQ ID NOS: 217
SOFTWARE: PatentIn Ver. 2.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 1710.5; DB 4 Pred. No. 9.1e-131;
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Best Local Similarity 90.9
Matches 321; Conservative
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                                                                                                                                                                                                                                                                         RESULT 5
US-09-800-729-145
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US-08-336-891-2
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DB 3; Length 483;
                                                                                                                                                                                                                                               APPLICANT: Yue, Henry
APPLICANT: Yue, Henry
APPLICANT: Au-Young, Janice
APPLICANT: Gorley, Neil C.
APPLICANT: Guegler, Karl J.
APPLICANT: Baughn, Mariah R.
TITLE OF INVENTION: HUMAN IMMUNE SYSTEM ASSOCIATED PROTEINS
CORRESPONDENCE: 28
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             12; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           OPERATING SYSTEM: OND TO CONTROLL OPERATING SYSTEM: DOS CURRENT APPLICATION DATA:
APPLICATION DATA:
APPLICATION NUMBER: US/09/049,672A
FILING DATE: HEREWITH
CLASSIFICATION: 536
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
ATTORNEY/AGENT INFORMATION:
NAME: CERTONE, Michael C
REGISTRATION NUMBER: 39,132
REFERENCE/DOCKET NUMBER: 39,132
REFERENCE/DOCKET NUMBER: 39,132
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650-865-0555
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 1710.5; DB Pred. No. 9e-131; 7; Mismatches 1
                                                                                                                                                                                                                                                                                                                                                                       STREET: 3174 Porter Drive CITY: Palo Alto
                                                                                                                        Sequence 5, Application US/09049672A Patent No. 6135941 GENERAL INFORMATION:
                                                                                                                                                                                        Hillman, Jennifer L.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   90.1%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COMPUTER: IBM Compatible OPERATING SYSTEM: DOS
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SEQUENCE CHARACTERISTICS:
LENGTH: 483 amino acids
TYPE: amino acid
STRANDEDNESS: single
                                                                                                                                                                                                            Lal, Preeti
Tang, Y. Tom
Yue, Henry
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Conservative
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MEDIUM TYPE: Diskette
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            IMMEDIATE SOURCE:
LIBRARY: BMARNOT03
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Best Local Similarity
Matches 321; Conserv
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; CLONE: 1669829
US-09-049-672A-5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             USA
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                                                                                                       US-09-049-672A-5
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NEW JERSEY
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Sequence 4, Application PC/TUS9513795

GENERAL INFORMATION:

APPLICANT: PATEL, MAYUR D.

TITLE OF INVENTION: DNA BNCODING CANINE IMMUNOGLOBULINS

TITLE OF INVENTION: DNA BNCODING CANINE IMMUNOGLOBULINS

TOWNBER OF SEQUENCES: 4

CORRESPONDENCE ADDRESS:

ADDRESSEE: CHRISTINE E. CARTY

STREET: 126 E. LINCOLN AVENUE; P.O. BOX 2000

CITY: RAHWAY
                                                                       COUNTRY: USA

COUNTRY: USA

COUNTRY: USA

COUNTRY: USA

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IEM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/336,891
FILING DATE: 09-NOV-1994
CLASSIFICATION: 424
ATTORNEY/AGENT INFORMATION:
NAME: CARTY, CHRISTINE E.
REGISTRATION NUMBER: 19340
TELEPHONE: (908) 594-6734
TELEPHONE: (908) 594-4720
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 33 amino acide
TYPE: amino acide
TYPE: AMINO acide
STRANDEDNESS: single
               3: CHRISTINE E. CARTY
126 E. LINCOLN AVENUE; P.O. BOX 2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TOPOLOGY: linear
MOLECULE TYPE: protein
CORRESPONDENCE ADDRESS
                                                            RAHWAY
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match 66.8%; Score 1267.5; DB 5; Length 343; Best Local Similarity 67.0%; Pred. No. 5.3e-95; Matches 236; Conservative 38; Mismatches 69; Indels 9;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        292 AEDWKQGEKFSCMVGHEALPMSFTQKTIDRLAGKPTHVNVSVVMAEVDGICY
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Sequence 4, Application US/08399106A
Patent No. 573168
GENERAL INFORMATION:
APPLICANT: Carter, Paul J.
APPLICANT: Ridgway, John B.
TITLE OF INVENTION: A METHOD FOR MAKING HETEROMULTIMERIC TITLE OF INVENTION: POLYPEPTIDES
NUMBER OF SEQUENCES: 16
CORRESPONDENCE ADDRESS:
ADDRESSEE: Genentech, Inc.
STREET: 460 Point San Bruno Blvd
CITY: South San Francisco
STATE: California
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IEM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PAtentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US95/13795
FILING DATE:
                                                                                                                                                                                                                                                         CLASSIFICATION:
ATTORNEY/AGRAT INFORMATION:
NAME: CARTY, CHRISTINE
REGISTRATION NUMBER: 36,09
REFERENCE/DOCKET NUMBER: 19211Y
TELECOMMUNICATION INFORMATION:
TELEPHONE: (908) 594-6734
TELEPAX: (908) 594-4720
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             LENGTH: 343 amino acids TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STRANDEDNESS: single
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MOLECULE TYPE: protein
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0; Gaps

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223 GNTERPEVHLLPPPSEELALNELVTLTCLARGESPRDVLVRWLQGSQELPREKYLTWASR 282
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 4, Application US/08434869A

Sequence 4, Application US/08434869A

Patent No. 5521333

GENERAL INFORMATION:

APPLICANT: Carter, Paul J.

APPLICANT: Presta, Leonard G.

APPLICANT: Ridgway, John B.

TITLE OF INVENTION: A METHOD FOR MAKING HETEROMULTIMERIC POLYPEPTIDES

NUMBER OF SEQUENCES: 16

CORRESPONDENCE ADDRESS:

ADDRESSEE: Genentech, Inc.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 GNTFRPQVHLLPPPSEELALBZLVTLTCLARGFSPRDVLVRWLQGSQELPREKYLTWASR
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Pred. No. 3.2e-40;
4; Mismatches 0; Indels
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MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
COMPUTER: 1BM FC comparible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: WinPatin (Genentech)
CURRENT APPLICATION DATA:
APPLICATION DATA:
APPLICATION NUMBER: US/08/434,869A
FILING DATE: 03-May-1995
CLASSIFICATION DATA:
APPLICATION NUMBER: 08/399106
FILING DATE: 01-MR-1995
ATTORNEY/AGENT INFORMATION:
NAME: Lee, Wendy M:
NA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STREET: Genentech, Inc.
STREET: 460 Point San Bruno Blvd
CITY: South San Francisco
STATE: California
COUNTRY: USA
ZIP: 94080
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TELECOMMUNICATION INFORMATION:
TELEPHONE: 415/225-1994
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Best Local Similarity 96.5%;
Matches 109; Conservative
                             TELEFAX: 415/952-9881
TELEX: 910/371-7168
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                          113 amino acids
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Best Local Similarity 96:5
Matches 109; Conservative
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TELEPHONE:
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                                                                                                                                                                      LENGTH:
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Patent No. 5807706
GENERAL INFORMATION:
APPLICANT: Carter, Paul J.
APPLICANT: Ridgway, John B.
TITLE OF INVENTION: A METHOD FOR MAKING HETEROMULTIMERIC POLYPEPTIDES
NUMBER OF SEQUENCES: A METHOD FOR MAKING HETEROMULTIMERIC POLYPEPTIDES
NUMBER OF SEQUENCES: A METHOD FOR MAKING HETEROMULTIMERIC POLYPEPTIDES
NUMBER OF SEQUENCES: A METHOD FOR MAKING HETEROMULTIMERIC POLYPEPTIDES
STAFET: 460 Point San Bruno Blvd
CITY: South San Bruno Blvd
CITY: California
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 GNTFRPQVHLLPPPSEELALBZLVTLTCLARGFSPKDVLVRWLQGSQELPREKYLTWASR
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
30.8%; Score 585; DB 1; Length 113;
Best Local Similarity 96.5%; Pred. No. 3.2e-40;
Matches 109; Conservative 4; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COMPUTER READBLE FORM:
MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
COMPUTER: 1BM PC computable
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: WinPatin (Genentech)
CURRENT APPLICATION DATA:
APPLICATION PATE:
APPLICATION MAY:
APPLICATION ADMS:
APPLICATION DATE: 03-May-1995
CLASSIFICATION: 530
                                                                                         COMPUTER: 3.5 inch, 1.44 Mb floppy disk COMPUTER: 3.5 inch, 1.44 Mb floppy disk COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS SOFTWARE: Winbatin (Genentech) CURRENT APPLICATION DATA: US/08/399,106A FILLING DATE: US/WENTION: NAME: Lee, Wendy REGISTRATION NUMBER: 00,000 REGISTRATION NUMBER: P0927 TELECOMMUNICATION: TELECOMMUNICATION: TELEPHONE: 415/225-1994
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                P0927D2
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CLASSIFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/399106
FILING DATE: 01-MAR-1995
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       REGISTRATION NUMBER: 00,000
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TELEX: 910/371-7168
INFORMATION FOR SEQ ID NO: 4: SEQUENCE CHARACTERISTICS:
                                                                      COMPUTER READABLE FORM:
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79 AGKSVTCHVKH-----YTNPSQDVTVPCPVPSTPPTPSPSTPPTPSPSCCHPRL 127
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                                                                                                                                                                                                                                  Sequence 2, Application PC/TUS9105826
GENERAL INPORMATION:
APPLICANT: Soulillou, Jean-Paul
TITLE OF INVENTION: Protein Polyligands Joined To A Stable Protein
TITLE OF INVENTION: Core
NUMBER OF SEQUENCES: 11
CORRESPONDENCE ADDRESS:
                                                                      300 VAAEDWKKGDTFSCMVGHEALPLAFTQKTIDRLAGKPTHVNVSVVMAEVDGTCY
                                                                                                 ; Score 505; DB 5; Length 504; Pred. No. 7.2e-33; 49; Mismatches 131; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US91/05826
FILING DATE: 19910822
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    242 SQSMFTCRVDHRGLTFQQNASSMCVPDQDTAI----
                                                                                                                                                                                                                                                                                                                                                                                                 ADDRESSEE: Bertram I. Rowland, Ph.D. STREET: 4 Embarcadero Center, Suite 3400 CITY: San Francisco STATE: California COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         REFERENCE/DOCKET NUMBER: FP55352-1/BIR
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-781-1989
TELEFAX: 415-494-8771
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/575,394
FILING DATE: 29-AUG-1990
ATTORNEY/AGENT INFORMATION:
NAME: REGISTRATION NUMBER: 20,015
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ZIP: 94111
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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Best Local Similarity 33.3%;
Matches 118; Conservative 49
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AMINO ACID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TOPOLOGY: linear
MOLECULE TYPE: protein
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183 LICQATGFSPRQ-IQVSWLREGKQVGSGVTTDQVQAEAKESGPTTYKVTSTLTIKESDWL 211
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1 GNTFRPQVHLLPPPSEELALBZLVTLTCLARGFSPKDVLVRWLQGSQELPREKYLTWASR
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                                                                                                                                                                                                       Sequence 2, Application US/07932915
Patent No. 5672486
GENERAL INFORMATION:
APPLICANT: Soulillow, Jean-Paul
TITLE OF INVENTION: Core
NUMBER OF SEQUENCES: 11
CORRESPONDENCE ADDRESS:
ADDRESSEE: Cooley Godward Castro Huddleson & Tatum
                                                                           283 QEPSQGTTTFAVTSILRVAAEDWKKGDTFSCMVGHEALPLAFTQKTIDRLAGK 335
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26.6%; Score 505; DB 1; Length 50
Best Local Similarity 33.3%; Pred. No. 7.2e-33;
Matches 118; Conservative 49; Mismatches 131; Indels
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5 Palo Alto Square, Suite 400
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/646,875
FILING DATE: 28-JAN-1991
APPLICATION NUMBER: US 07/575,394
FILING DATE: 23-AUG-1990
ATTORNEY/AGENT INFORMATION:
REGISTRATION NUMBER: 20,015
REFRENCE/DOCKET NUMBER: 20,015
REFRENCE/DOCKET NUMBER: ATLA-001/01US
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION 18-691-0663
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APPLICATION NUMBER: US/07/932,915
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COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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TOPOLOGY: line
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STATE: California
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Length 504;

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120; Conservative
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Matches 120; Conservative
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ORGANISM: Sus sp.
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Matches
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TITLE OF INVENTION: Antigenized Antibody Vaccine for Foot-and-Mouth Disease
FILE REFERENCE: 09/291,299
CURRENT APPLICATION NUMBER: US/09/291,299A
CURRENT FILING DATE: 1999-04-15
NUMBER OF SEQ ID NOS: 22
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 1.
                                                                                                                                                                                APPLICANT: Yong, Xie TILE OF INVENTION: Antigenized Antibody Vaccine for Foot-and-Mouth Disease TILE OF INVENTION: Antigenized Antibody Vaccine for Foot-and-Mouth Disease CURRENT APPLICATION NUMBER: US/09/291,299A CURRENT FILING DATE: 1999-04-15 SOFTWARE; Patentin Vor. 2.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              143 CPGCEVAGPSVFIFPPKPKDTLMISQTPEVTCVVVDVSKEHAEVQPSWYVDGVEVHTAET 202
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  203 RPKEEQFNSTYRVVSVLPIQHQDWLKGKEFKCKVNNVDLPAPITRTISKAIGQSREPQVY 262
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 263 TLPPPAEELSRSK-VTLTCLVIGFYPPDIHVEWKSNGQPEPENTYRTTPPQQDVD---GT 318
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SGDLYTTSSQLTLPATQCLAGKSVTCHVKH-YTNPSQDVTVPCPVPSTPPTPSPSTPPTP 118
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          119 SPSC--CHPRLSLHRPALEDLILGSEA-NLTCTLTGL-RDASGVTFTWTPSSGK--SAVQ 172
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           173 GPPDRDLCGCYSVSSVLSGCAEPWNHGKTFTCTAAYPESKTPLTATLSKS-GNTFRPEVH 231
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        94 SG-LYSLSSMVTVPASS-LSSKSYTCNVNHPATTTKVDKRVGIHQPQTCPI-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         35 APKTAPSVYPLAPCGRDVSGPNVALGCLASSYFP-EPVTVTWNSGALTSGVHTFPSVLQP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                   25; Gaps
            Query Match 23.4%; Score 444.5; DB 4; Length 362; Best Local Similarity 34.9%; Pred. No. 3.8e-28; Matches 120; Conservative 48; Mismatches 151; Indels 25
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                                                                                                                               Sequence 6, Application US/09291299A
Patent No. 6774225
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        US-09-291-299A-1
, Sequence 1, Application US/09291299A
, Patent No. 6774225
, GENERAL INFORMATION:
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Best Local Similarity
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ORGANISM: Sus sp.
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ORGANISM: Sus sp.
-09-291-299A-1
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LENGTH: 362
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Sequence 3, Application US/09291299A

Sequence 3, Application US/09291299A

Patent No. 6774225

GENERAL INFORMATION:

APPLICANT: Yong, Xie

TITLE OF INVENTION: Antigenized Antibody Vaccine for Foot-and-Mouth Disease

FILE REFERENCE: 09/291,299

CURRENT APPLICATION NUMBER: US/09/291,299A

CURRENT FILING DATE: 1999-04-15

NUMBER OF SEQ ID NOS: 22

SOFTWARE: Patentin Ver. 2.1

SEQ ID NO 3
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48; Mismatches 151; Indels
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Sequence 48, Appl Sequence 48, Appl Sequence 4058, Ap Sequence 4058, Ap Sequence 4245, Ap Sequence 4245, Ap Sequence 738, App Sequence 3773, Ap Sequence 3773, Ap Sequence 3778, Ap Sequence 3778, Ap
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                                                                                                                                                                             October 25, 2005, 11:07:58 ; Search time 131.252 Seconds (without alignments) 1555.504 Million cell updates/sec
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2: /cgn2_6/ptodata/2/pubpaa/PCT NEW PUB.pep:*
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GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.
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ALIGNMENTS

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US-10-644-256-3
US-10-644-256-3
US-10-644-256-3
US-10-644-256-3
Publication No. US20050106722A1
Sequence 3, Application US/10644256
Publication No. US20050106722A1
GENERAL INFORMATION:
APPLICAMY: Douts. David HA
APPLICAMY: Bout. Abraham
ITILE OF INVENTION: Efficient Production of 1gA in Recombinant Mammalian Cells
ITILE OF INVENTION: Efficient Production of 1gA in Recombinant Mammalian Cells
CURRENT PILIAG DATE: 2003-08-20
PRIOR PRIOR PELICATION NUMBER: US 60/129,463
PRIOR PILING DATE: 1999-04-15
PRIOR PILING DATE: 1999-04-15
NUMBER OF SEC 1D NOS: 8
SCFTWARE: PatentIn version 3.2
SEC 1D NO 3
LENGTH: 489
TYPE: PT
ORGANISM: artificial
FEATURE:
NAME/KEY: MISC_FEATURE
LOCATION: (1).__(21)
OTHER INFORMATION: Amino acid sequence anti-EpCAM 1gA heavy chain
FEATURE:
NAME/KEY: MISC_FEATURE
LOCATION: (1).__(21)
OTHER INFORMATION: Leader peptide
FEATURE:
NAME/KEY: MISC_FEATURE
LOCATION: (22)...(136)
OTHER INFORMATION: UN Region
FEATURE:
NAME/KEY: MISC_FEATURE
LOCATION: (137)...(238)
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Best Local Similarity
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Sequence 48, 499 lication US/10422628

Publication No. US20040014174A1

GENERAL INFORMATION:

APPLICANT: THE SCRIPPS RESEARCH INSTITUTE

APPLICANT: FRANKLIN, Scett E.

TITLE OF INVENTION: EXPRESSION OF POLYPEPTIDES IN CHLOROPLASTS, AND COMPOSITIONS AND TITLE OF INVENTION: EXPRESSION OF POLYPEPTIDES IN CHLOROPLASTS, AND COMPOSITIONS AND TITLE OF INVENTION: EXPRESSION OF POLYPEPTIDES IN CHLOROPLASTS, AND COMPOSITIONS AND TITLE OF INVENTION: EXPRESSION OF POLYPEPTIDES IN CHLOROPLASTS, AND COMPOSITIONS AND TITLE OF INVENTION NUMBER: US 60/375,129

PRIOR PELLING DATE: 2003-04-23

PRIOR FILING DATE: 2002-04-23

PRIOR FILING DATE: 2002-12-19

NUMBER OF SEQ ID NOS: 48

SOFTWARE: Patentin version 3.1

SEQ ID NO 48
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Pred. No. 7.5e-147;
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LOCATION: (239)..(359)
OTHER INFORMATION: CH2 Region
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NAME/KEY: MISC_FEATURE
LOCATION: (360)..(489)
OTHER INFORMATION: CH3 Region
OTHER INFORMATION: CH1 Region
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             373
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               254 SPASPTSPKVPPLSLCSTQPDGNVVIACLVQGFFPQEPLSVTWSESGQGVTARNPPPSQD 313
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                                                                                                                                                                                                                                                            Length 630;
                                                                                                                                                                                                                                                                                                                                                           Indels
                                                                                                                                                                                                                                                  Query Match 89.4%; Score 2335; DB 15;
Best Local Similarity 92.4%; Pred. No. 2.3e-130;
Matches 439; Conservative 11; Mismatches 15;
ORGANISM: Artificial sequence
FEATURE:
OTHER INFORMATION: Single-chain atibody
US-10-422-628-48
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ORGANISM: Artificial sequence
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Length 639

Score 2335; DB 15; Pred. No. 2.3e-130;

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199 SQDASGDLYTTSSQLTLPATQCLAGKSVTCHVKHYTNPSQDVTVPCPVPSTPPTPSPSTP 258
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        259 PTPSPSCCHPRLSLHRPALEDLLLGSEANLTCTLTGLRDASGVTFTWTPSSGKSAVQGPP 318
                                                                    FTWTPSSGKSAVQGPPDRDLCGCYSVSSVLSGCAEPWNHGKTFTCTAAYPESKTPLTATL 355
                                                                                      303 FTWTPSSGKSAVQGPPERDLCGCYSVSSVLPGCAEPWNHGKTFTCTAAYPESKTPLTATL 362
                                                                                                                                                                                                          ASRQEPSQGTTTFAVTSILRVAAEDWKKGDTFSCMVGHEALPLAFTQKTIDRLAGKPTHV 475
                                                                                                                                                                                                                            423 ASRQEPSQGTTTFAVTSILRVAAEDWKKGDTFSCMVGHEALPLAFTQKTIDRLAGKPTHV 482
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PTPSPSCCHPRISLHRPALEDLILGSEANLTCTLTGLRDASGVTFTWTPSSGKSAVQGPP 311
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                     243 PCPVPSTPPTPSPSTPTPSPSCCHPRLSLHRPALEDLLLGSEANLTCTLTGLRDASGVT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match 87.4%; Score 2281.5; DB 15; Length 496; Best Local Similarity 90.0%; Pred. No. 2.6e-127; Matches 430; Conservative 13; Mismatches 26; Indels 9;
                                                                                                                                                                                                                                                                                                                                                                                               Sequence 3006, Application US/10104047
; Bublication No. US20030236392A1
; GENERAL INFORMATION:
; FAPLICANT: HELIX RESEARCH INSTITUTE
; TITLE OF INVENTION: No. US20030236392A1e1 full length cDNA
; FILE REPERENCE: H1-A0105
; CURRENT APPLICATION NUMBER: US/10/104,047
; CURRENT FILING DATE: 2002-03-25
; PRIOR APPLICATION NUMBER:
; PRIOR FILING DATE:
; NUMBER OF SEQ ID NOS: 4096
; SOFTWARE: Patentin Ver. 2.1
                                                                                                                                                                                                                                                                                                   483 NVSVVMAEVDGTCY 496
                                                                                                                                                                                                                                                                               476 NVSVVMAEVDGTCY 489
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ORGANISM: Homo sapiens
US-10-104-047-3006
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US-10-104-047-3006
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                        85 FOGRVTITADESTSTAYMELSSLRSEDTAVYYCARDPF------LHYWGQGTLVTV 134
                                                                                                                                                                      135 STASPISPKVFPLSLCSTOPDGNVVIACLVQGFFPQEPLSVTWSESGQGVTARNFPPSQD 194
                                                                                                                                                                                                                                                                                                              255 SPSCCHPRLSLHRPALEDLLLGSEANLTCTLTGLRDASGVTFTWTPSSGKSAVQGPPDRD 314
                                                                                                                                                                                                                                                                                                                                                                                    LCGCYSVSSVLSGCAEPWNHGKTFTCTAAYPESKTPLTATLSKSGNTFRPEVHLLPPPSE 374
                                                                                                                                                                                                                                                                                                                                                                                                                                                       ELALNELVTLTCLARGESPKDVLVRWLQGSQELPREKYLTWASRQEPSQGTTTFAVTSIL 434
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          120 ----DPFLHYWGOGTLVTVSTASPTSPKVFPLSLCSTQPDGNVVIACLVQGFFPQEPLSV 175
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                                                                                                                                                                                                                                                             323 ASGDLYTTSSQLTLPATQCLAGKSVTCHVKHYTNPSQDVTVPCPVPSTPPTPSPSTPTP
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                                  25 LVQSGAEVKKPGSSVRVSCKASGGTFSSYAISWVRQAPGQGLEWMGGIIPIFGTANYAQK
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   10; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match 88.2%; Score 2302; DB 15; Length 496; Best Local Similarity 87.9%; Pred. No. 1.6e-128; Matches 434; Conservative 22; Mismatches 24; Indels 14; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          435 RVAAEDWKKGDTFSCMVGHEALPLAFTQKTIDRLAGKPTHVNVSVVMAEVDGTCY 489
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ; Sequence 4058, Application US/10108260A; Bublication No. US20040005560A1; GENERAL INFORMATION:
; APPLICANT: HELIX RESEARCH INSTITUTE
; TITLE OF INVENTION: No. US20040005560A1e1 full length cDNA; FILE REFERENCE: H1-A0106; CURRENT FILIATION: No. US20040005560A1e1 full length cDNA; CURRENT FILIATION: S. 2002-03-27; NUMBER OF SEQ ID NOS: 5458; SOFTWARE: Patentin Ver. 2.1; SEQ ID NO 4058; LENGTH: 496
   15; Indels
 11; Mismatches
 439; Conservative
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ORGANISM: Homo sapiens
US-10-108-260A-4058
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81 YAQKFQGRVTITADESTSTAYMELSSLRSEDTAVYYCARDPFLH------YWGQGTLV 132
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        304 ASGVIFTWTPSSGKSAVQGPPERDLCGCYSVSSVLPGCAEPWNHGKTFTCTAAYPESKTP 363
                                                                                                                                                                                                                                                                         66 LEWNGGIIPIFGTANYAQKFQGRVTITADESTSTAYMELSSLRSEDTAVYYCA-RDP--- 121
                                                                                                                                                                                                                                                                                               124 IDLSCFTSGVYGLGLWGQGTWVWVSSASPTSPKVFPLSLCSTQPDGNVVIACLVQGFFPQ 183
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    LTATLSKSGNTFRPEVHLLPPPSEELALNELVTLTCLARGFSPKDVLVRWLQGSQELPRE 410
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        KYLTWASRQEPSQGTTTFAVTSILRVAAEDWKKGDTFSCMVGHEALPLAFTQKTIDRLAG 470
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                     184 EPLSVTWSESGQGVTARNFPPSQDASGDLYTTSSQLTLPATQCLAGKSVTCHVKHYTNPS
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                                                                                                                                                                                                             -----PLHYWGQGTLVTVSTASPTSPKVFPLSLCSTQPDGNVVIACLVQGFFPQ
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                291 ASGVTFTWTPSSGKSAVQGPPDRDLCGCYSVSSVLSGCAEPWNHGKTFTCTAAYPESKTP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       21 AQVQLVQSGAEVKKPGSSVRVSCKASGGTFSSYAISWVRQAPGQGLEWMGGIIPIFGTAN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 4277, Application US/10108260A
Publication No. US20040005560A1
GENERAL INFORMATION:
APPLICANT HELLY RESEARCH INSTITUTE
APPLICANTION: No. US20040005560A1e1 full length cDNA
FILE REFERENCE: H1-A0106
CURRENT APPLICATION NUMBER: US/10/108,260A
CURRENT APPLICATION NUMBER: US/202-03-27
NUMBER OF SEQ ID NOS: 5458
SOFTWARE: ParentIn Ver. 2.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   85.4%; Score 2230; DB 15;
87.8%; Pred. No. 3e-124;
                                                                                                 87.1%; Score 2275; DB 15;
87.2%; Pred. No. 6.5e-127;
ative 16; Mismatches 30;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       , Pred. No. 3e-1
18; Mismatches
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                                                                                                                                             Matches 435; Conservative
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Matches 419; Conservative
                                     ; ORGANISM: Homo sapiens
US-10-108-260A-4245
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                                                                                                   Query Match
Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     374 EELALNELVTLTCLARGESPKDVLVRWLOGSQELPREKKLTWASRQEPSQCTTTRAVTSI 433
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                VSTASPTSPKVFPLSLCSTQPDGNVVIACLVQGFFPQEPLSVTWSESGQGVTARNFPPSQ 193
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   314 DLCGCYSVSSVLSGCAEPWNHGKTFTCTAAYPESKTPLTATLSKSGNTFRPEVHLLPPPS 373
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                79
                                       496
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DASGDLYTTSSQLTLPATQCLAGKSVTCHVKHYTNPSQDVTVPCPVPSTPPTPSPSTPPT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PSPSCCHPRLSLHRPALEDLLLGSEANLTCTLTGLRDASGVTFTWTPSSGKSAVQGPPDR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       22 QVQLVQSGAEVKKPGSSVRVSCKASGGTFSSYAISWVRQAPGQGLEWMGGIIPIFGTANY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SILRVAAEDWKKGDTFSCMVGHEALPLAFTQKTIDRLAGKPTHVNVSVVMAEVDGTCY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length 495;
                                                                                                                              Sequence 4065. Application US/10108260A; Publication No. US20040005560A1; GENERAL INFORMATION:

APPLICANT: HELLIX RESEARCH INSTITUTE
TITLE OF INVENTION:
CURRENT APPLICATION NO. US20040005560A1e1 full length cDNA
CURRENT APPLICATION NUMBER: US/10/108,260A
NUMBER OF SEQ ID NOS: 5458
SOFTWARE; PARENTIN Ver. 2.1
SEQ ID NO 4085
LENGTH: 495
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PUBlication No. US2004005560A1
GENERAL INFORMATION:
APPLICANT: HELLY RESEARCH INSTITUTE
TITLE OF INVENTION: No. US20040005560A1e1 full length cDNA
FILLE REFERENCE: H1-A0106
CURRENT APPLICATION NUMBER: US/10/108,260A
CURRENT FILING DATE: 2002-03-27
NUMBER OF SEQ ID NOS: 5438
SOFTWARE: PATENTIN Ver. 2.1
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89.7%; Pred. No. 5.6e-127;
tive 17; Mismatches 24;
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Best Local Similarity 89.79
Matches 427; Conservative
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                                                                                                   RESULT 6
US-10-108-260A-4085
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US-10-108-260A-4245
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65 GLEWMGGIIPIFGTANYAQKFQGRVTITADESTSTAYMELSSLRSEDTAVYYCARDPF-- 122
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        123 ----LHYWGQGTLVTVSTASPTSPKVFPLSLCSTQPDGNVVIACLVQGFFPQEPLSVTW 177
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                123 AICYGFSPWGQGTLVTVSSASPTSPKVFPLSLCSTQPDGNVVIACLVQGFFPQEPLSVTW 182
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    183 SESGQGVTARNFPPSQDASGDLYTTSSQLTLPATQCLAGKSVTCHVKHYTNPSQDVTVPC 242
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      243 PVPSTPPTPSPSTPPTPSPSCCHPRLSLHRPALEDLLLGSEANLTCTLTGLRDASGVTFT 302
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          303 WIPSSGKSAVGEPPERDLCGCYSVSSVLPGCAEPWNHGKTFTCTAAYPESKTPLTATLSK 362
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          178 SESGQGVTARNFPPSQDASGDLYTTSSQLTLPATQCLAGKSVTCHVKHYTNPSQDVTVPC 237
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PVPSTPPTPSPSTPPTPSPSCCHPRLSLHRPALEDLLLGSEANLTCTLTGLRDASGVTFT 297
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                WTPSSGKSAVQGPPDRDLCGCYSVSSVLSGCAEPWNHGKTFTCTAAYPESKTPLTATLSK 357
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         363 SGNTFRPEVHLLPPPSEELALNELVTLTCLARGFSPKDVLVRWLQGSQELPREKYLTWAS 422
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               4 GLRWVFLVA-FLEGVQCEVQLVESGGGLVKPGGSLRLSCAASGLSFSTYAMNWVRQAPGK 62
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PRIOR FILING DATE: 2001-02-05
PRIOR APPLICATION NUMBER: 60/267,057
PRIOR PILING DATE: 2001-02-07
PRIOR FILING DATE: 2001-02-07
PRIOR APPLICATION NUMBER: 60/266,975
PRIOR FILING DATE: 2001-02-07
PRIOR FILING DATE: 2001-02-08
Remaining Prior Application data removed - See File Wrapper or PALM.
SEPTWARE: PETENTIN Ver. 2.1
SEC ID NO 798
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GENERAL INFORMATION:
TITLE OF INVENTION: NO. US20030236392A1el
TITLE OF INVENTION: NO. US20030236392A1el full length cDNA
TITLE OF INVENTION: NO. US20030236392A1el full length cDNA
TITLE OF INVENTION: NO. US20030236392A1el full length cDNA
CURRENT APPLICATION NUMBER:
PRIOR PELLING DATE: 2002-03-25
PRIOR PELLING DATE:
NUMBER OF SEQ ID NOS: 4096
SOFTWARE: PATENTION VET: 2.1
SOFTWARE: PATENTION VET: 2.1
SEQ ID NO 3773
LENGTH: 497
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84.8%; Score 2215; DB 15;
Best Local Similarity 84.8%; Pred. No. 2.3e-123;
Matches 417; Conservative 26; Mismatches 41;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        478 SVVMAEVDGTCY 489
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US-10-072-012-798
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US-10-104-047-3773
                                                                                                                                                                                                                                                                                  LENGTH: 494
TYPE: PRT
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FPPEFLDRVILERDTSASTVYMELASLTSEDSALYYCARGTPLRMETEFAXDVWGQGTRV 138
                                                                                                                                                                              QDASGDLYTTSSQLTLPATQCLAGKSVTCHVKHYTNPSQDVTVPCPVPSTPPTPSPRTPP 252
                                                                                                                                                                                                     TPSPSCCHPRLSLHRPALEDLLLGSEANLTCTLTGLRDASGVTFTWTPSSGKSAVQGPPD 31.2
                                                                                                         SEELALNELVTLTCLARGFSPKDVLVRWLQGSQELPREKYLTWASRQEPSQCTTTFAVTS 438
                                                                            TVSTASPISPKVFPLSLCSTQPDGNVVIACLVQGFFPQEPLSVTWSESGQGVTARNFPPS 192
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     373 SEBLALNELVTLTCLARGFSPKDVLVRWLQGSQELPREKYLTWASRQEPSQGTTTFAVTS 432
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: Snimkets, Kichard
APPLICANT: Snimkets, Kichard
APPLICANT: Gangolli, Esha
APPLICANT: Gangolli, Esha
APPLICANT: Padigaru, Muralidhara
APPLICANT: Rastelli, Luca
APPLICANT: Rastelli, Luca
APPLICANT: Rastelli, Luca
APPLICANT: Gerlach, Valeries E.
APPLICANT: Gerlach, Valeries E.
APPLICANT: Gerlach, Valeries E.
APPLICANT: Golman, Steven D.
APPLICANT: Grosse, William M.
APPLICANT: Alsobrook II, John P.
APPLICANT: Alsobrook II, John P.
APPLICANT: Alsobrook II, John P.
APPLICANT: Burges, Catherine E.
ITLE OF INVENTION: Proteins and Nucleic Acids Encoding Same FILE REFERENCE: 2140-228
CURRENT APPLICATION NUMBER: US/10/072,012
PRIOR APPLICATION NUMBER: 60/265,102
PRIOR APPLICATION NUMBER: 60/265,517
PRIOR APPLICATION NUMBER: 60/265,517
PRIOR APPLICATION NUMBER: 60/265,317
PRIOR PILING DATE: 2001-01-31
PRIOR PILING DATE: 2001-01-31
PRIOR PILING DATE: 2001-01-31
PRIOR APPLICATION NUMBER: 60/266,406
PRIOR PILING DATE: 2001-01-31
PRIOR APPLICATION NUMBER: 60/266,767
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Publication No. US20040033493A1
GENERAL INFORMATION:
APPLICANT: Tchernev, Velizar
APPLICANT: Spytek, Kimberly
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Patturajan, Meera
Shimkets, Richard
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KHYTNPSQDVTVPCPVPSTPPTSPSTPPTPSPSCCHPRLSLHRPALEDLLLGSEANLTC 283
   GLEWV-SVIYANGDTYYAASVKGRFTISRDNSENALYLQMNSLRVEDAAVYYCVRNYYDS
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81.0%; Pred. No. 7.2e-122;
tive 28; Mismatches 46; Indels 22
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Publication No. US20030236392A1

GENERAL INFORMATION:

APPLICANT: HELIX RESEARCH INSTITUTE

TITLE OF INVENTION: No. US20030236392A1e1 full length cDNA

FILE REFERENCE: H1-A0105

CURRENT APPLICATION NUMBER: US/10/104,047

CURRENT FILING DATE: 2002-03-25

PRIOR APPLICATION NUMBER:

PRIOR APPLICATION NUMBER:

SEQ ID NOS: 4096

SEQ ID NOS: 4096

SEQ ID NOS: 233
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Matches 410; Conservative
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                                                                                                                                                                                        65 GLEWMGGIIPIFGT-AN---YAQKFQGRVTITADESTSTAYMELSSLRSEDTAVYYCARD 120
                                                                                                                                                                                                                                                        121 PF-----LHYWGQGTLVTVSTASPTSPKVFPLSLCSTQPDGNVVIACLVQGFFPQ 170
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                                                                                                                                             4 GLNW--VVLAALLRGVQCQVQLVESGGGVVQPGTSLRLSCVVSGFTFTNFPMHWLRQAPGK 62
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Publication No. US20040005560A1
GENERAL INFORMATION:
TITLE OF INVENTION: No. US20040005560A1e1 full length cDNA FILE REFERENCE: H1-A0106
CURRENT APPLICATION NUMBER: US/10/108,260A
NUMBER OF SEQ ID NOS: 5458
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 4078
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Best Local Similarity 84.0%; Pred. No. 5.3e-122;
Matches 414; Conservative 26; Mismatches 43;
                                                                84.3%; Score 2200.5; DB 1:
83.2%; Pred. No. 1.7e-122;
                                                                                             31, Mismatches
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                                                              Query Match
Best Local Similarity 83.25
Matches 415; Conservative
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-104-047-3773
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ORGANISM: Homo sapiens
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US-10-108-260A-4078
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120 123 NLGVAWIVAGPGNVRPRKWFDSWGQGTLVAVSSPSPTSPKVFPLSLCSTQPDGNVVIACL 182 296 356 163 223 242 301 361 416 476 481 62 64 63 GLEWVSSTAASGANTFYADSVKGRFTVSRDNSENMMYLQMSSLRGEDTGIYYCAKDGDVP GLEWMGGIIPIFGTANYAQKFQGRVTITADESTSTAYMELSSLRSEDTAVYYCARD----183 VQGFFPQEPLSVTWSESGQGVTARNFPPSQDASGDLYTTSSQLTLPATQCLAGKSVTCHV SGFSTAIDYWGQGSLVIVTSASPTSPKVFPLSLCSTQPDGNVVIACLVQGFFPQEPLSVT WSESGOGVTARNFPPSQDASGDLYTTSSQLTLPATQCLAGKSVTCHVKHYTNPSQDVTVP WSESGGOVTARNFPPSQDASGDLYTTSSQLTLPATQCLAGKSVTCHVKHYTNPSQDVTVP 242 CPVPSTPPTPSPSTPPTPSPSCCHPRLSLHRPALEDLILGSEANLTCTLTGLRDASGVTF TWTPSSGKSAVQGPPDRDLCGCYSVSSVLSGCAEPWNHGKTFTCTAAYPESKTPLTATLS KSGNTFRPEVHLLPPPSEELALNELVTLTCLARGFSPKDVLVRWLQGSQELPREKYLTWA SRQEPSQGTTTFAVTSILRVAAEDWKKGDTFSCMVGHEALPLAFTQKTIDRLAGKPTHVN SRQEPSQGTTTFAVTSILRVAAEDWKKGDTFSCAVGHEALPLAFTQKTIDRLAGKPTHVN 5 GFLWALVISTCLEFSMAQVQLVQSGAEVKKPGSSVRVSCKASGGTFSSYAISWVRQAPGQ 121 ------PFLHYWGQGTLVTVSTASPTSPKVFPLSLCSTQPDGNVVIACL 164 VQGFFPQEPLSVTWSESGQGVTARNFPPSQDASGDLYTTSSQLTLPATQCLAGKSVTCHV CPVPSTPPTPSPSTPPSPSCCHPRLSLHRPALEDLLLGSEANLTCTLTGLRDASGVTF KSGNTFRPEVHLLPPPSEELALNELVTLTCLARGFSPKDVLVRWLQGSQELPREKYLTWA

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FEATURE:
NAME/KEY: SITE
LOCATION: (488)
OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
LOCATION: (490)
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OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
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Best Local Similarity 83.9%; Pred. No. 1.3e-121;
Matches 412; Conservative 21; Mismatches 50;
                                                                                                                                                     Sequence 112, Application US/09800729
Patent No. US20020068319A1
GENERAL INFORMATION:
APPLICATURE NI et al.
TITLE OF INVENTION:
FILE REFREENCE: PF044P1
CURRENT APPLICATION NUMBER: US/09/800,729
CURRENT FILING DATE: 2001-03-08
PRIOR APPLICATION NUMBER: PCT/US00/26013
PRIOR APPLICATION NUMBER: 60/155,709
PRIOR APPLICATION NUMBER: 60/155,709
PRIOR FILING DATE: 1999-09-24
PRIOR FILING DATE: 1999-09-24
NUMBER OF SEQ ID NOS: 217
SOFTWARE: PatentIn Ver: 2.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         OTHER INFORMATION: Xaa equals any of the
  475 VNVSVVMAEVDGTCY 489
                               483 VNVSVVMAEVDGTCY 497
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TYPE: PRT
ORGANISM: Homo sapiens
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LOCATION: (505)
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LOCATION: (494
                                                                                                                 RESULT 14
US-09-800-729-112
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                                                                                                                                                              363 YPESKTPLTATLSKSGNTFRPEVHLLPPPSEELALNELVTLTCLARGFSPKDVLVRWLQG 422
                                                                                                                                                                                                                                                       423 SQELPREKYLTWASRQEPSQCTTTFAVTSILRVAAEDWKKGDTFSCWVGHEALPLAFTQK 482
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       363 LSKSGNTFRPEVHLIPPPBEELALNELVTLTCLARGFSPKDVLVRWLQGSQBLPREKYLT 422
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                                                                                                                                                                                                                                  SQELPREKYLTWASRQEPSQGTTTFAVTSILRVAAEDWKKGDTFSCMVGHEALPLAFTQK
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 4244, Application US/10108260A
Publication No. US20040005560A1
GENERAL INFORMATION:
APPLICANT: HELIX RESEARCH INSTITUTE
TITLE OF INVENTION: No. US20040005560A1e1 full length cDNA
FILE REPRESENCE: H1-A0106
CURRENT APPLICATION NUMBER: US/10/108,260A
CURRENT FILING DATE: 2002-03-27
NUMBER OF SEQ ID NOS: 5458
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 4244
                                                                                                                                                                                                                                                                                                                   TYPE: PRT
ORGANISM: Homo sapiens
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LOCATION: (490)
OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
NAME/KEY: SITE
LOCATION: (494)
OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
NAME/KEY: SITE
LOCATION: (495)
OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
NAME/KEY: SITE
NAME/KEY: SITE
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                                       477
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LOCATION: (488)
OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
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363 SGNTFRPEVHLLPPPSEELALNELVTLTCLARGFSPKDVLVRWLQGSQELPREKYLTWAS 422
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SESGQGVTARNFPPSQDASGDLYTTSSQLTLPATQCLAGKSVTCHVKHYTNPSQDVTVPC 237
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                                                           423 RQEPSQGTTTFAVTSILRVAAEDWKKGDTFSCMVGHEALPLAFTQKTIDRLAGKPTHVNV
                                       418 RQEPSQGTTTFAVTSILRVAAEDWKKGDTFSCMVGHEALPLAFTQKTIDRLAGKPTHVNV
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Publication No. US20040010134A1
GENERAL INFORMATION:
TITLE OF INVENTION:
FILE REFERENCE:
CURRENT FILING DATE: 2001-04-12
PRIOR PEPIGATION NUMBER: 60/229, 358
PRIOR APPLICATION NUMBER: 60/229, 358
PRIOR PELING DATE: 2000-04-12
PRIOR FILING DATE: 2000-12-21
PRIOR PILING DATE: 2000-12-21
PRIOR PILING DATE: 2000-12-21
PRIOR PILING DATE: 2000-12-21
PRIOR FILING DATE: 2000-04-15
NUMBER OF SEQ ID NOS: 2267
SEQ ID NO 2189
SEQ ID NO 2189
LENGTH: 530
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Matches 412; Conservative
                                                                                                                   478 SVVMAEVDGTC 488
                                                                                                                                           483 SVVMAXVXGPC 493
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ORGANISM: Homo sapiens
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US-09-833-245-2189
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                                  WTPSSGKSAVQGPPDRDLCGCYSVSSVLSGCAEPWNHGKTFTCTAAYPESKTPLTATLSK 357
                                                                                                                                          422
243 PVPSTPPTPSPSTPPTPSPSCCHPRLSLHRPALEDLLLGSEANLTCTLTGLRDASGVTFT 302
                                                       SGNTFRPEVHILLPPPSEELALNELVTLTCLARGFSPKDVLVRWLOGSOELPREKYLTWAS
                                                                                                          SGNTFRPEVHILPPPSEELALNELVTLTCLARGFSPKDVLVRWLQGSQELPREKYLTWAS
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Search completed: October 25, 2005, 11:27:10 Job time : 134.252 secs

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Result No.

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FEATURE:
NAME/KEY: SITE
LOCATION: (488)
NAME/KEY: SITE
LOCATION: Xaa equals any of the naturally occurring L-amino acids
NAME/KEY: SITE
LOCATION: (490)
OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
NAME/KEY: SITE
LOCATION: (491)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ; LOCATION: (505)
; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
US-09-800-729-112
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83.7%; Score 2186; DB 4; Length 530;
Best Local Similarity 83.9%; Pred. No. 9.7e-154;
Matches 412; Conservative 21; Mismatches 50; Indels
                                                                                                                                                                                                                                                                                                                                                                                                            GENERAL INFORMATION:

APPLICANT: Ni et al.

TITLE OF INVENTION: 32 Human secreted proteins
FILE REFERENCE: P2044P1
CURRENT APPLICATION NUMBER: US/09/800,729
CURRENT FILING DATE: 2001-03-08
FRICR APPLICATION NUMBER: BCT/US00/26013
FRICR APPLICATION NUMBER: 60/155,709
FRICR FILING DATE: 1999-09-24
SOFTWARE: RetentIN Ver. 2.0

SEQ ID NO 112

LENGTH: 530
US-09-472-087-68
US-09-488-7378-67
US-10-071-488-67
US-07-994-373C-23
US-08-477-6428-23
US-08-147-6428-23
US-09-705-686-23
US-09-705-392-23
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US-09-705-392-23
US-09-405-718-90
US-09-416-247-7
US-09-472-087-66
US-09-472-087-66
US-09-077-48-71
US-09-077-48-71
US-09-077-48-800-12
US-09-077-48-10
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Patent No. 6605592
GENERAL INFORMATION:
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NAME/KEY: SITE
LOCATION: (495)
OTHER INFORMATION: Xaa equals
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ORGANISM: Homo sapiens
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                 GenCore version 5.1.6
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US-09-049-672A-1

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US-09-316-891-2

PCT-US95-1378-39-10

US-09-627-896B-24

US-09-627-896B-24

US-09-627-896B-24

US-09-472-896B-24

US-08-458-516-13

US-08-458-516-13

US-08-472-898A-7

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Maximum Match 100%
Listing first 45 summaries
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Maximum DB seq
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243 PVPSTPPTPSPSTPPTPSPSCCHPRLSLHRPALEDLLLGSEANLTCTLTGLRDASGATFT 302
                                       WIPSSGKSAVQGPPDRDLCGCYSVSSVLSGCAEPWNHGKTFTCTAAYPESKTPLTATLSK 357
                                                                                                                                                    363 SGNTFRPEVHLLPPPSEELALNELVTLTCLARGFSPKDVLVRWLQGSQELPREKYLTWAS
                                                                                                                                                                                                              RQEPSQCTTTFAVTSILRVAAEDWKKGDTFSCMVGHEALPLAFTQKTIDRLAGKPTHVNV
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                                                                SGNTFRPEVHLLPPPSEELALNELVTLTCLARGFSPKDVLVRWLQGSQELPREKYLTWAS
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APPLICANT: Hillman, Jennifer L.
APPLICANT: Tang, Y. Tom
APPLICANT: Yee, Henry
APPLICANT: Yee, Henry
APPLICANT: Gorley, Neil C.
APPLICANT: Guegler, Karl J.
APPLICANT: Baughn, Mariah R.
TITLE OF INVENTION: HUMAN IMMUNE SYSTEM ASSOCIATED PROTEINS
CORRESPONDENCE: 28
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length 499;
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MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSEQ for Windows Version 2.0
SUFTWARENT APPLICATION DATA:
APPLICATION NUMBER: US/09/049,672A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SSEE: Incyte Pharmaceuticals, Inc. : 3174 Porter Drive Palo Alto
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 78.6%; Score 2053;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NAME: Cerrone, Michael C
REGISTRATION NUMBER: 39,137
REFERENCE/DOCKET NUMBER: P
TELECOMMUNICATION INFORMATION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            FILING DATE: HEREWITH
CLASSIFICATION: 536
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                LENGTH: 499 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                              478 SVVMAEVDGTCY 489
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CLONE: 021145
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STATE: CA
COUNTRY: USI
ZIP: 94304
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JAPPLICANT: Ni et al.
TITLE OF INVENTION: 32 Human secreted proteins; FILE REFERENCE: PSO44P1; CURRENT APPLICATION NUMBER: US/09/800,729; CURRENT FILING DATE: 2001-03-08; PRIOR PELICATION NUMBER: PCT/US00/26013; PRIOR APPLICATION NUMBER: PCT/US00/26013; PRIOR APPLICATION NUMBER: 60/155,709; PRIOR FILING DATE: 1999-09-24; NUMBER OF SEQ ID NOS: 217; SOFTWARE: Patentin Ver. 2.0; SEQ ID 0216; LENGTH: 494
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Matches 408; Conserv
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US-09-800-729-216
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RESULT 5
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                                                                                10 LVISTCLEFSMAQVQLVQSGAEVKKPGSSVRVSCKASGGTFSS--YAISWVRQAPGQGLE
                                                                                                                                    68 WMGGIIPIFGTANYAQKFQGRVTITADESTSTAYMELSSLRSEDTAVYYCAR-----
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APPLICANT: Lal, Preeti
APPLICANT: Lal, Preeti
APPLICANT: Yea, Y. Tom
APPLICANT: Yea, Henry
APPLICANT: Au-Young, Janice
APPLICANT: Gorley, Neil C.
APPLICANT: Guegler, Karl J.
APPLICANT: Baughn, Mariah R.
TITLE OF INVENTION: HUMAN IMMUNE SYSTEM ASSOCIATED PROTEINS
CORRESPONDENCE ADDRESS:
  ilarity 78.3%; Pred. No. 6.2e-144;
Conservative 35; Mismatches 51;
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MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOPTWARE: FastSEQ for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/049,672A
FILING DATE: HEREWITH
CLASSIFFCATION: 536
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ADDRESSEE: Incyte Pharmaceuticals, Inc
STREET: 3174 Porter Drive
CITY: Palo Alto
STATE: CA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 5, Application US/09049672A Patent No. 6135941 GENERAL INFORMATION:
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Best Local Similarity
Matches 389; Conserv
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US-09-049-672A-5
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length 483;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           55; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
76.8%; Score 2004.5; DB 3;
Best Local Similarity 77.5%; Pred. No. 2.3e-140;
Matches 383; Conservative 33; Mismatches 55;
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FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Cerrone, Michael C
REGISTRATION NUMBER: 39,132
REFERENCE/DOCKET NUMBER: PF-0497 US
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650-855-0555
TELEFAX: 650-845-4166
                                                                                                                                                                                                                                                                     SEQUENCE CHARACTERISTICS:
| LENGTH: 483 amino acids
| TYPE: amino acid
| TYPE: amino acid
| STRANDEDNESS: single
| TOPOLOGY: linear |
| TOPOLOGY: linear |
| LIBRARY: BMARNOT03 |
| CLONE: 1669829 |
                                                                                                                                                                                                                                                 INFORMATION FOR SEQ ID NO: 5:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  476 NVSVVMAEVDGTCY 489
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APPLICATION NUMBER: US/08/336,891
FILING DATE: 09-NOV-1994
CLASSIFICATION: 424
ATTORNEY AGENT INFORMATION:
NAME: CARTY, CHRISTINE E.
REGISTRATION NUMBER: 36,099
REFERENCE/DOCKET NUMBER: 19340
TELEPHONE: (908) 594-6734
TELEPHONE: (908) 594-6734
TELEPHONE: (908) 594-6734
TELEPHONE: (908) 594-6736
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 343 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ATTORNEY/AGENT INFORMATION
                                                                                                                                                                                                                                                                                                                                        MOLECULE TYPE: protein
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           FILING DATE:
                                                                                                                                                                                                                                                                                                                                                              US-08-336-891-2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         120 HRATRDGYQLEYRGFDYWGQGILVTVSSASPTSPKVFPLSLDSTPQDGNVVVACLVQGFF 179
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           180 PQEPLSVTWSESGQNVTARNFPPSQDASGDLYTTSSQLTLPATQCPDGKSVTCHVKHYTN 239
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    289 RDASGVTFTWTPSSGKSAVQGPPDRDLCGCYSVSSVLSGCAEPWNHGKTFTCTAAYPESK 348
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  349 TPLTATLSKSGNTFRPEVHLLPPPSEELALNELVTLTCLARGFSPKDVLVRWLQGSQELP 408
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                                                                                                                                                                                                                                                                                                                     287 RDASGATFTWTPSSGKSAVQGPPERDLCGCYSVSSVLPGCAQPWNHGETFTCTAAHPELK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               169 PQEPLSVTWSESGQGVTARNFPPSQDASGDLYTTSSQLTLPATQCLAGKSVTCHVKHYTN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               229 PSQDVTVPCPVPSTPPTPSPSTPPTPSPSCCHPRLSLHRPALEDLLLGSEANLTCTLTGL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            240 PSQDVIVPCPVP------PPPPPCCHPRLSLHRPALEDLLLGSEANLTCTLTGL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    407 REKYLTWASRQEPSQGTTTFAVTSILRVAAEDWKKGDTFSCWVGHEALPLAFTQKTIDRL
                                                                                                                                                                                                                                                                                           7 LW-ALVISTCLEPSMAQVQLVQSGAEVKKPGSSVRVSCKASGGTFSS--YAISWVRQAPG
                                                                                                                                                                                                                                                                                                                                                                                                                                                               124 H-----YWGQGTLVTVSTASPISPKVFPLSLCSTQPDGNVVIACLVQGFF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         347 TPLTANITKSGNIFRPEVHLLPPPSEELALNELVILICLARGFSPKDVLVRWLQGSQELP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    REKYLTWASRQEPSQGTTTFAVTSILRVAAEDWKKGDTFSCMVGHEALPLAFTQKTIDRL
                                                                                                                                                                                                                                                        Gaps
                                                                                                                                                                                                                                                      35;
                                                                                                                                                                                                               4; Length 487;
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; Patent No. 5622842
; GENERAL INFORMATION:
; APPLICANT: HOLLIS, GREGORY F.
; APPLICANT: PATEL, MAYUR D.
; TITLE OF INVENTION: DNA ENCODING CANINE IMMUNOGLOBULIN A NUMBER OF SEQUENCES: 2
; CORRESPONDENCE ADDRESS: 3
; ADDRESSEE: CHRISTINE E. CARTY
; STREET: 126 E. LINCOLN AVENUE; P.O. BOX 2000
; CITY: RAHWAY
; STATE: USA
                                                                                                                                                                                                           Query Match 75.5%; Score 1970.5; DB 4; Length Best Local Similarity 76.0%; Pred. No. 7.7e-138; Matches 381; Conservative 31; Mismatches 54; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ZIP: 07065-0900
ZIP: 07065-0900
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
PRIOR APPLICATION NUMBER: 60/155,709
PRIOR FILING DATE: 1999-09-24
NUMBER OF SEQ ID NOS: 217
SOFTWARE: PatentIN Ver. 2.0
SEQ ID NO 145
LENGTH: 487
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                                                                                                                         TYPE: PRT
ORGANISM: Homo sapiens
US-09-800-729-145
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258 CCHPRLSLHRPALEDLLLGSEANLTCTLTGLRDASGVTFTWTPSSGKSAVQGPPDRDLCG 317
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 LNELVTLTCLVRGFKPKDVLVRWLQGTQELPQEKYLTWEPLKEPDQ-TNMFAVTSMLRVT 291
                                                                                                                                                                      138 SPISPKVFPLSLCSTQPDGNVVIACLVQGFFPQEPLSVTWSESGQGVTARNFPPSQDASG
                                                                                                                                                                                                                                                                                            61 SLYTMSSQLTLPAAQCPDDSSVKCQVQHASSPSKAVSVPC-----KDNSHPCHPCPS
                                                                                                                                                                                                                                                                                                                                                                                                                     113 CNEPRISIQKPALEDLIJGSNASLTCTLSGLKDPKGATFTWNPSKGKEPIQKNPERDSCG
                                                                                                                                                                                                                                                        198 DLYTTSSQLTLPATQCLAGKSVTCHVKHYTNPSQDVTVPCPVPSTPPTPSPSTPPTPSPS
                                                                 Gaps
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                                                              9
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; Sequence 4, Application PC/TUS9513795
; GENERAL INFORMATION:
; APPLICANT: HOLLIS, GREGORY F.
; APPLICANT: PATEL, MAYUR D.
; TITLE OF INVENTION: DNA ENCODING CANINE IMMUNOGLOBULINS; NUMBER OF SEQUENCES: 4
; CORRESPONDENCE ADDRESS:
ADDRESSEE: CHRISTINE E. CARTY
STREET: 126 E. LINCOLN AVENUE; P.O. BOX 2000
CITY: RAHMAY
; STATE: NEW JERSEY
; COUNTRY: USA
   DB 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ZIP: 07065-0907

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATR:
APPLICATION NUMBER: PCT/US95/13795
Query Match
48.5%; Score 1267.5; DB
Best Local Similarity 67.0%; Pred. No. 5.1e-86;
Matches 236; Conservative 38; Mismatches 69
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232

28;

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APPLICANT: RUP, BÖNITA
APPLICANT: VELDMAN, GEERTRUIDA M.
TITLE OF INVENTION: HUMANIZED IMMUNOGLOBULIN REACTIVE WITH B7-2 AND METHODS
TITLE OF INVENTION: OF TREATMENT THEREWITH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             405 DIAVEMESINGO--PENNYKTTPPVLD-SDG--SFPLYSKLTVDKSRWQQGNVFSCSVMHE 459
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     66 LEWMGGIIPIFGTANYAQKFQGRVTITADESTSTAYMELSSLRSEDTAVYYCARDPF--- 122
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              64 LEWMGGIIPLFGTPTYSQNFQGRVTITADKSTSTAHMELTSLRSEDTAVYYCATDRYRQA 123
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       -----LHYWGQGTLVTVSTASPTSPKVFPLSLCS-TQPDGNVVIACLVQGFFPQEP 172
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                173 LSVTWSESGQGVTARNFPPSQDASGDLYTTSSQLTLPATQCLAGKSVTCHVKHY-TNPSQ 231
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 232 DVTV------PCPVPSTPPTPSPST-PPTPSPSCCHPRLSLHRPALEDLLLGSE 278
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 241 DKKVEPKSCDKTHTCPPCPAPELLGGPSVFLFPPKPK---------DTLMISRT 285
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                279 ANLTCTLTGL-RDASGVTFTWTPSSGK--SAVQGPPDRDLCGCYSVSSVLSGCAEPWNHG 335
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           286 PEVICVVVDVSHEDPEVKENWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNG 345
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                336 KTFTCTAAYPESKTPLTATLSKS-GNTFRPEVHLLPPPSEELALNELVTLTCLARGFSPK 394
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                      7 FLFVVAAAATGVQ---SQMQVVQSGAEVKKPGSSVTVSCKASGGTFSNYAISWVRQAPGQG 63
                                                                                                                                                                                                                                                                                                                                                                                                                                        6 FLWALVISTCLEFSMAQVQLVQSGAEVKKPGSSVRVSCKASGGTFSSYAISWVRQAPGQG
                                                                                                                                                                                                                                                                                                                                                                                        69; Mismatches 161; Indels
                                                                                                                                                                                                                                                                                                                                           Query Match 33.7%; Score 880; DB 2; Best Local Similarity 42.1%; Pred, No. 3.6e-57;
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APPLICANT: CO, MAN SUNG
APPLICANT: VASQUEZ, MAXIMILIANO
APPLICANT: CARRENO, BEATRIZ
APPLICANT: CLINIKER, ABBIE CHERYL
APPLICANT: GOLLINS, MARY
APPLICANT: GOLDNAN, SAMUEL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ; Sequence 24, Application US/09627896B; Patent No. 6827934
  NAME: ERNST, BARBARA G
REGISTRATION NUMBER: 30,377
REFERENCE/DOCKET NUMBER: 180
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 783-6040
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       460 ALHNHYTOKSLSLSPGK 476
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                                                                                                                      TELEFAX: (202) 783-6031
INFORMATION FOR SEQ ID NO: 10:
SEQUENCE CHARACTERISTICS:
LENGTH: 476 amino acids
TYPE: amino acid
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KNIGHT, ANDREA
O'HARA, DENISE
                                                                                                                                                                                                                                                                                                                                                                                           Matches 209; Conservative
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MOLECULE TYPE: protein
US-08-378-939-10
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                    138 SPTSPKVFPLSLCSTQPDGNVVIACLVQGFFPQEPLSVTWSESGQGVTARNFPPSQDASG 197
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 198 DLYTTSSQLTLPATQCLAGKSVTCHVKHYTNPSQDVTVPCPVPSTPPTPSPSTPPTPSPS 257
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CYSVSSVLSGCAEPWNHGKTFTCTAAYPESKTPLTATLSKSGNTFRPEVHLLPPPSEELA 377
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             LNELVTLTCLARGFSPKDVLVRWLQGSQELPREKYLTWASRQEPSQGTTTFAVTSILRVA 437
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                                                                                                                                                                                                                                                                                                                                                                       Length 343;
                                                                                                                                                                                                                                                                                                                                                                                                                    69; Indels
                                                                                                                                                                                                                                                                                                                                                                    DB 5;
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CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/378,939
                                                                                                                                                                                                                                                                                                                                                                  Query Match 48.5%; Score 1267.5; DB Best Local Similarity 67.0%; Pred. No. 5.1e-86; Matches 236; Conservative 38; Mismatches 69
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT: CROWE, JAMES SCOTT
APPLICANT: LEWIS, ALAN PETER
TITLE OF INVENTION: PRODUCTION OF ANTIBODIES
NUMBER OF SEQUENCES: 46
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ADDRESSEE: ROTHWELL, FIGG, ERNST & KURZ STREET: 555 THIRTEENTH ST. N.W. CITY: WASHINGTON STATE: D. C. COUNTRY: U.S.
NAME: CARTY, CHRISTINE E.
REGISTRATION NUMBER: 36,099
REFERENCE/DOCKET NUMBER: 19211Y
TELECOMMUNICATION INFORMATION:
TELEPRAX: (908) 594-6734
TELEPRAX: (908) 594-6734
INFORMATION:
SEQUENCE CHARACTERISTICS:
LENGTH: 343 amino acids
TYPE: amino acids
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CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/952640
FILING DATE: 01-DEC-1992
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COMBUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      US-08-378-939-10
; Sequence 10, Application US/08378939
Patent No. 5876961
; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                              MOLECULE TYPE: protein
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APPLICANT: Tauji, Takashi
APPLICANT: Tauji, Takashi
APPLICANT: Tauji, Takashi
APPLICANT: Tauji, Takashi
APPLICANT: Tauzuka, Katsunari
APPLICANT: Hori, No. 6803039uaki
TITLE OF INVENTION: HUMAN MONOCLONAL ANTIBODY AGAINST A
TITLE OF INVENTION: COSTINULATORY SIGNAL TRANSDUCTION MOLECULE AILIM AND
TITLE OF INVENTION: PHARMACEUTICAL USE THEREOF
FILE REFERENCE: 06501-079001
CURRENT APPLICATION NUMBER: US/09/859,053
CURRENT FILING DATE: 2001-03-30
PRIOR APPLICATION NUMBER: UP 2001-99508
PRIOR PRILING DATE: 2001-03-30
PRIOR PRILING DATE: 2000-05-18
NUMBER OF SEQ ID NOS: 43
NUMBER OF SEQ ID NOS: 43
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                                                                                                                                                                                                                                                                                                                                                                                                                                            140 TSPKVFPLSLCS-TQPDGNVVIACLVQGFFPQEPLSVTWSESGQGVTARNFPPSQDASGD 198
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        305 SAVQGPPDRDLCGCYSVSSVLSGCAEPWNHGKTFTCTAAYPESKTPLTATLSKS-GNTFR 363
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                                                                                                                                                                                                                                                     Gaps
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                                                                                                                                                                                                                                                     Indels
                                                                                                                                                                                                           32.7%; Score 853.5; DB 4;
41.9%; Pred. No. 3.2e-55;
tive 70; Mismatches 161;
FILE REFERENCE: 08702.0081-01000
CURRENT APPLICATION NUMBER: US/09/627,896B
CURRENT FILING DATE: 2000-07-27
NUMBER OF SEQ ID NOS: 32
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO. 24
LENGTH: 462
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Patent No. 6803039
                                                                                                                                                                                                         Query Match
Best Local Similarity 41.9°
Matches 196; Conservative
                                                                                                                                TYPE: PRT; ORGANISM: 3D1 heavy chain US-09-627-896B-24
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CRGANISM: Homo sapiens
US-09-859-053-28
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US-09-859-053-28
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LENGTH: 470
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                                                                                                                                                                                                                                                                                                   TLVTVSTASPTSPKVFPLSLCS-TQPDGNVVIACLVQGFFPQEPLSVTWSESGQGVTARN 188
                                                                                                                                                                                                                                                                                                                             297 QFNWYVDGVEVHNAKTKPREEQFNSTFRVVSVLTVVHQDWLNGKEYKCKVSNKGLPAPIE 356
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                                                                                                                             255 ---APPVAGPSVFLFPPKPK--------DTLMISRTPEVTCVVVDVSHEDPEV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       295 TFTWTPSSGK--SAVQGPPDRDLCGCYSVSSVLSGCAEPWNHGKTFTCTAAYPESKTPLT
                                                    Gaps
                                                 57;
  Length 470;
                                                                                                                                                                                                                                                                                                                                                                                                      FPPSQDASGDLYTTSSQLTLPATQCLAGKSVTCHVKHY-TNPSQDVTV-
                                              Indels
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STREET: One Market Plaza, Steuart Tower, Suite 2000
CITY: San Francisco
STATE: California
COUNTRY: USA
                                                                                                                                                                                                81 YAQKFQGRVTITADESTSTAYMELSSLRSEDTAVYYCAR--
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Version #1.25
  DB 4;
                          ; Pred. No. 4.2e-54; 64; Mismatches 159;
32.1%; Score 838.5; 41.7%; Pred. No. 4.20
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REGISTRATION NUMBER: 30,223
REFERENCE/DOCKET NUMBER: 11823-37-3
TELECOMMUNICATION:
TELEPHONE: 415-326-2400
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ZIF: 94105
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PACEDIIN Release #1.0, Ve:
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/458,516
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APPLICATION NUMBER: US 08/059,159
FILING DATE: 03-MAY-1993
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 13, Application US/08458516
Patent No. 5777085
REDERRAL INFORMATION:
APPLICANT: Co, Man Sung
APPLICANT: TSo, J. Yun
TTTLE OF INVENTION: Humanized Antik
TITLE OF INVENTION: GPIIB/IIIA
NUMBER OP SEQUENCES: 23
NUMBER OP SEQUENCES: 23
CORRESPONDENCE ADDRESS:
ADDRESSEE: William M. Smith
                       Best_Local Similarity 41.7%
Matches 200; Conservative
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CLASSIFICATION: 424
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                                                                                                                                               19
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  Query Match
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81 YAQKFQGRVTITADESTSTAYMELSSLRSEDTAVYYCARD-----PFLHYWGQGTLVT 133
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           198 LOSSG-LYSLSSVVTVPSSS-LGTKTYTCNVDHKPSNTKVDKRVESKYGPPCP---SCPA 252
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             19 SQVQLQESGAEVKKPGASVKVSCKASGYTFTSYVIHWVRQAPGQGLEWIGYINPYNDGTD 78
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Patent No. 6165745
GENERAL INFORMATION:
APPLICANT: Ward, E. Sally
APPLICANT: Kim, Jin-Kyoo
TITLE OF INVENTION: Recombinant Production of
TITLE OF INVENTION: Immunoglobin-Like Domains in Prokaryotic Cells
NUMBER OF SEQUENCES: 33
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                                                                                                      PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/US91/08843
APPLICATION NUMBER: PCT/US91/08843
CLASSIFICATION: 424
APPLICATION: WINBER: 07/618.542
FILING DATE: No. 5871732ember 27, 1990
CLASSIFICATION: 424
                                                                                                                                                                                                                                                                                                                                                    ATTORNEY/AGENT INFORMATION:
NAME: JOHN J. MC DONNELL
REGISTRATION NUMBER: 26,949
REFERENCE/DOCKET NUMBER: 92,310-G
TELECOMMUNICATION INFORMATION:
TELEPHONE: (312) 715-1000
TELER: 910/221-5317
TELER: 910/221-5317
TELER: 910/221-5317
TELER: 910/221-5317
SEQUENCE CHARACTERISTICS:
                                           July 24, 1992
J: 424
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amino acid
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Best Local Similarity 40.8%
Matches 194; Conservative
                                           FILING DATE: Ju
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Patent No. 5871732
GENERAL INFORMATION:
APPLICANT: BURKLY, LINDA C.
APPLICANT: THOMAS, DAVID W.
APPLICANT: THOMAS, DAVID W.
APPLICANT: ROSA, WARGARET D.
APPLICANT: ROSA, WARGARET D.
APPLICANT: ROSA, WARGARET D.
APPLICANT: ROSA, WARGARET D.
APPLICANT: ROSA, MARGARET D.
APPLICANT: ROSA, WARGARET D.
APPLICANT: ROSA, MARGARET S.
APPLICANT: ROSA, MARGARET S.
APPLICANT: ROSA, MARGARET R.
APPLICANTING R.
APPLICANTIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      121 STKGPSVFPLAPSSKSTSGGTAALGCLVKDYFP-EPVTVSWNSGALTSGVHTFPAVLQSS 179
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         283 GVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAK 342
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                82 AQKFQGRVTITADESTSTAYMELSSLRSEDTAVYYCARDP----FLHYWGQGTLVTVSTA 137
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SPTSPKVFPLSLCS-TQPDGNVVIACLVQGFFPQEPLSVTWSESGQGVTARNFPPSQDAS 196
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GDLYTTSSQLTLPATQCLAGKSVTCHVKHY-TNPSQDVTV------PCPVPSTP 243
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        244 PTPSPST-PPTPSPSCCHPRLSLHRPALEDLLLGSEANLTCTLTGL-RDASGVTFTWTPS 301
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              238 GGPSVFLFPPKPK-------DTLMISRTPEVTCVVVDVSHEDPEVKFNWYVD 282
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   302 SGK--SAVQGPPDRDLCGCYSVSSVLSGCAEPWNHGKTFTCTAAYPESKTPLTATLSKS- 358
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           359 GNTFRPEVHLLPPPSEELALNELVTLTCLARGFSPKDVLVRWLQGSQELPREKYLTWASR 418
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       81
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               22 QVQLVQSGAEVKKPGSSVRVSCKASGGTFSSYAISMVRQAPGQGLEWMGGIIPIFGTANY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 OVQLVQSGAEVKKPGSSVKVSCKASGYAFTNYLIEWVRQAPGQGLEWIGVIYPGSGGTNY
                                                                                                                                                                                                                                                                                                                                                        Query Match 31.7%; Score 828.5; DB 1; Length 449;
Best Local Similarity 41.9%; Pred. No. 2.2e-53;
Matches 198; Conservative 64; Mismatches 164; Indels 47; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              419 QEPSQGTTTFAVTSILRVAAEDWKKGDTFSCMVGHEALPLAFTOKTIDRLAGK 471
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OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: WORD PERFECT 5.1
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
                                                                                                             LENGTH: 449 amino acids
TELEFAX: 415-326-2422
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                       TYPE: amino acid
STRANDEDNESS: single
                                                                                                                                                                                                                ; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-458-516-13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STATE: ILLINOIS COUNTRY: U.S.A.
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81 YAQKFQGRVTITADESTSTAYMELSSLRSEDTAVYYCAR------DFFLHYWGQGTLV 132
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TVSTASPTSPKVFPLSLCS-TQPDGNVVIACLVQGFFPQEPLSVTWSESGQGVTARNFPP 191
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PPTPSPSCCHPRLSLHRPALEDLLLGSEANLTCTLTGL-RDASGVTFTWTPSSGK--SAV 307
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  21 AQVQLVQSGAEVKKPGSSVRVSCKASGGTFSSYAISWVRQAPGQGLEWMGGIIPIFGTAN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          24 SQVQLVQSGAEVKKPGSSVKVSCKASGGTFSSYAISWVRQAPGQGLEWMGGIIPIFGTAN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SQDASGDLYTTSSQLTLPATQCLAGKSVTCHVKHYTNPSQDVTVPCPVPSTPPTPSPT-
                         417 SRQEPSQGTTTFAVTSILRVAAEDWKKGDTFSCMVGHEALPLAFTQKTI 465
                                                     396 PVLD-SDG--SFFLYSKLTVDKSRWQEGNVFSCSVMHEALHNHYTQKSL 441
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          30.8%; Score 803; DB 4; Length 442; 42.4%; Pred. No. 1.7e-51; Live 57; Mismatches 151; Indels
                                                                                                                                                                                                                                                                                         TITLE OF INVENTION: AGP-ANTIBODY FUSION PROTEINS
TITLE OF INVENTION: AND RELATED MOLECULES AND METHODS
UNMBER OF SEQUENCES: 9
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COMPUTER READBLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: Diskette
COMPUTER: Diskette
OPERATING SYSTEM: DOS
SOFTWARE: FastSEG for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/472,888A
FILING DATE: 07-JUN-1995
CLASSIFICATION: 424
PRIOR APPLICATION: 424
PRIOR APPLICATION NUMBER: 07/618,314
FILING DATE: 23-NOV-1990
ATTORNEY/AGENT INFORMATION:
NAME: ELBİNG, KAREN KAREN
REFERENCE/DOCKET NUMBER: 35,238
REFERENCE/DOCKET NUMBER: 00786/258001
                                                                                                                                                                            Sequence 7, Application US/08472888A Patent No. 6613746 GENERAL INFORMATION:
APPLICANT: Seed, Brian APPLICANT: Walz, Gerd
                                                                                                                                                                                                                                                                                                                                                                                  E: Clark & Elbing LLP
176 Federal Street
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TELECOMMUNICATION INFORMATION:
TELEPHONE: 617-428-0200
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     LENGTH: 442 amino acids TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local Similarity 42.44
Matches 197; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE CHARACTERISTICS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TOPOLOGY: linear MOLECULE TYPE: protein
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                                                                                                                                                                                                                                                                                                                                                                                                                                 Boston
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STREET: 17
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                                                                                                                                                              US-08-472-888A-7
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             279 VDGVQVHNAKTKPREQQYBSTYRVVSVLTVLHQNWLDGKEYKCKVSNKALPAPIEKTISK 338
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           83 QKFQGRVTITADESTSTAYMELSSLRSEDTAVYYCARDPFLHYWG------QGTLVTVS 135
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 136 TASPTSPKVFPLSLCS-TQPDGNVVIACLVQGFFPQEPLSVTWSESGQGVTARNFPPSQD 194
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          195 ASGDLYTTSSQLTLPATQCLAGKSVTCHVKHY-TNPSQDVTV------PCPVPS 241
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  242 TPPTPSPST-PPTPSPSCCHPRLSLHRPALEDLLLGSEANLTCTLTGL-RDASGVTFTWT 299
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   234 LLGGPSVFLFPPKPK-------DTLMISRTPEVTCVVVDVSHEDPQVKFNWY 278
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         300 PSSGK--SAVQGPPDRDLCGCYSVSSVLSGCAEPWNHGKTFTCTAAYPESKTPLTATLSK 357
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               358 S-GNTFRPEVHLLPPPSEELALNELVTLTCLARGESPKDVLVRWLQGSQELPREKYLTWA 416
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        82
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     23 VQLVQSGAEVKKPGSSVRVSCKASGGTFSSYAISWVRQAPGQGLEWMGGIIPIFGTANYA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             55; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            31.3%; Score 817.5; DB 3; Length 445; 42.6%; Pred. No. 1.4e-52; ive 60; Mismatches 154; Indels 55
                                                                               STATE: Texas
COUNTRY: USA
ZIP: 7721-4133
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTIN Release #1.0, Version #1.30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /note= "Xaa = Pca (PCA:
pryollidonecarboxylic acid)'
                                                                                                                                                                                                                                                                                                          FILING DATE: 17-NOV-1994
CLASSIFICATION: 435
PRIOR PEPLICATION DATA:
APPLICATION NUMBER: US 07/963,333
FILING DATE: 19-OCT-1992
PROOR PAPLICATION NUMBER: US 07/873,930
FILING DATE: 24-APR-1992
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                           CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/341,560B
FILING DATE: 17-NOV-1994
                E: ARNOLD, WHITE & DURKEE P.O. Box 4433
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              UTSD:353
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NAME: Parker, David L.
REGLETRATION NUMBER: 32.165
REFERENCE/DOCKET NUMBER: UTSD
TELECOMMUNICATION INFORMATION:
TELEPAX: (713) 789-2679
INPORMATION FOR SEQ ID NO: 17:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               LENGTH: 445 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NAME/KEY: Modified-site
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
Best Local Similarity 42.69
Matches 200, Conservative
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    OTHER INFORMATION:
COTHER INFORMATION:
US-08-341-5608-17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TYPE: amino acid
STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TOPOLOGY: linear
                                         STREET: P.O. | CITY: Houston
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83

Gaps

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187 VLQSSG-LYSLSSVVTVPSSSDKKVEPKSCD-KTHTCP-----PCPAPELLGGPSVFLF 238
                          192 SQDASGDLYTTSSQLTLPATQCLAGKSVTCHVKHYTNPSQDVTVPCPVPSTPPTPSPST- 250
                                                                                                                                                                  PPTPSPSCCHPRLSLHRPALEDLLLGSEANLTCTLTGL-RDASGVTFTWTPSSGK--SAV 307
                                                                                                                                                                                                           239 PPKPK-------DTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAK 283
                                                                                                                                                                                                                                                     308 QGPPDRDLCGCYSVSSVLSGCAEPWNHGKTFTCTAAYPESKTPLTATLSKS-GNTFRPEV 366
                                                                                                                                                                                                                                                                                          284 TKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQV 343
                                                                                                                                                                                                                                                                                                                                      367 HLLPPPSEELALNELVTLTCLARGFSPKDVLVRWLQGSQELPREKYLTWASRQEPSQGTT 426
                                                                                                                                                                                                                                                                                                                                                                344 YILPPSRDELTKNQ-VSLTCLVKGFYPSDIAVEWESNGQ--PENNYKTTPPVLD-SDG-- 397
133 TVSTASPTSPKVFPLSLCS-TQPDGNVVIACLVQGFFPQEPLSVTWSESGQGVTARNFPP 191
                                                                                                                                                                                                                                                                                                                                                                                                                       427 TFAVTSILRVAAEDWKKGDTFSCMVGHEALPLAFTQKTIDRLAGK 471
                                                                                                                                                                                                                                                                                                                                                                                                                                                 398 SFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK 442
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  84 YAQKFQGRVTITADEST------ARDNGA-YCSGGSCYSGWFDP----WGQGTLV 127
  367 HLLPPPSEELALNELVTLTCLARGFSPKDVLVRWLQGSQELPREKYLTWASRQEPSQGTT 426
                                                                                                                                                                    344 YTLPPSRDELTKNQ-VSLTCLVKGFYPSDIAVEWESNGQ--PENNYKTTPPVLD-SDG-- 397
                                                               308 QGPPDRDLCGCYSVSSVLSGCAEPWNHGKTFTCTAAYPESKTPLTATLSKS-GNTFRPEV 366
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              21 AQVQLVQSGAEVKKPGSSVRVSCKASGGTFSSYAISWVRQAPGQGLEWMGGIIPIFGTAN 80
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            60; Gaps
                                                                                                                                                                                                                                                                                                                                                                Sequence 9, Application PC/TUS9610043
GENERAL INFORMATION:
APPLICANT: The General Hospital Corporation
TITLE OF INVENTION: P-SELECTIN LIGANDS AND RELATED MOLECULES
TITLE OF INVENTION: AND METHODS
NUMBER OF SEQUENCES: 14
CORRESPONDENCE ADDRESS:
ADDRESSEE: Fish & Richardson P.C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match 30.8%; Score 803; DB 5; Length 442; Best Local Similarity 42.4%; Pred. No. 1.7e-51; Matches 197; Conservative 57; Mismatches 151; Indels
                                                                                                                                                                                                                                                       SFPLYSKLTVDKSRWQQGNVFSCSVWHEALHNHYTQKSLSLSFGK 442
                                                                                                                                                                                                                                 TFAVTSILRVAAEDWKKGDTFSCMVGHEALPLAFTQKTIDRLAGK 471
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SOFTWARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US96/10043
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  REFERENCE/DOCKET NUMBER: 00786/284001
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617/542-5070
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/000,213
APPLICATION 14-UNN-1995
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: Lecth, Karen F.
REGISTRATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              E: Fish & Richardson P.C. 225 Franklin Street
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
CMPUTER: IEM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STRANDEDNESS: not relevant
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       INFORMATION FOR SEQ ID NO: 9: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  LENGTH: 442 amino acids
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ; MOLECULE TYPE: protein PCT-US96-10043-9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          amino acid
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COUNTRY: USA
ZIP: 02210-2804
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            FILING DATE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TELEFAX:
TELEX: 20
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